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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
An Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg./Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____
Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher D. Schreibe
Searcher Phone # 308-4292
Searcher Location CMC 6403
Date Searcher Picked Up _____
Date Completed 10/23
Searcher Prep & Review Time 14
Client Prep Time _____
Online Time 8

Type of Search

NA Sequence (#) 2
AA Sequence (#) _____
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel Orbit _____
Dr. Link _____
Lexis Nexis _____
Sequence Systems Compuserk
WWW Internet _____
Other (specify) _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 05:44:15 ; Search time 3600 Seconds
(without alignments)
12584.318 Million cell updates/sec

Title: US-09-868-987-1
Perfect score: 1864
Sequence: 1 atggacttcgcattatgtc.....atgacaaattcagataatgc 1864

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 452938

Minimum DB seq length: 5
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_pbg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	29.6	1.6	95	9 AI349643	AI349643 ta75h07.x
C 2	29.6	1.6	97	29 BZ378901	BZ378901 SALK_1121
C 3	28.2	1.5	79	28 BH97060	BH97060 3526_1_6
C 4	28	1.5	93	12 BJ055533	BJ055533 BJ055533

C	5	27.2	1.5	90	9 AI271303	AI271303 qw69902.x
C	6	27.2	1.5	99	9 AL667436	AL667436 AL667436
C	7	26.6	1.4	91	9 AW733398	AW733398 8K73A03.Y
C	8	26.6	1.4	97	9 AU061738	AU061738 AU061738
C	9	26.6	1.4	98	9 AV675896	AV675896 AV675896
C	10	26.6	1.4	100	13 BQ795262	BQ795262 EST_4200
C	11	26.4	1.4	76	28 AZ781137	AZ781137 2M0019C09
C	12	26.2	1.4	99	9 AI769234	AI769234 wg35605.x
C	13	26	1.4	80	9 AA647052	AA647052 vn39a11.x
C	14	26	1.4	80	29 AL938880	AL938880 Arabidops
C	15	26	1.4	91	9 AU263983	AU263983 AU263983
C	16	25.8	1.4	87	28 BH861222	BH861222 SALK_0348
C	17	25.8	1.4	93	29 CC326207	CC326207 RRJ093.Ba
C	18	25.8	1.4	98	9 AA683513	AA683513 zF34A09.B
C	19	25.8	1.4	100	12 BI938442	BI938442 des3b09.Y
C	20	25.6	1.4	76	28 BH791176	BH791176 SALK_0588
C	21	25.6	1.4	78	13 BU879460	BU879460 V060E04.P
C	22	25.6	1.4	87	28 AZ309857	AZ309857 1M0017M12
C	23	25.6	1.4	89	28 BH810836	BH810836 SALK_0512
C	24	25.6	1.4	94	12 BI692389	BI692389 603342884
C	25	25.6	1.4	95	28 BH850307	BH850307 SALK_0710
C	26	25.6	1.4	100	13 BX298804	BX298804 BX298804
C	27	25.4	1.4	81	9 AU013607	AU013607 AU013607
C	28	25.2	1.4	70	28 AZ789636	AZ789636 2M0037C09
C	29	25.2	1.4	79	14 CA330429	CA330429 haa98e07.
C	30	25.2	1.4	81	10 BF102955	BF102955 601646972
C	31	25.2	1.4	88	9 AU259801	AU259801 AU259801
C	32	25.2	1.4	91	29 CC459608	CC459608 SALK_1307
C	33	25.2	1.4	99	9 AA724210	AA724210 a109f07.8
C	34	25	1.3	86	28 AZ858741	AZ858741 2M0164K03
C	35	25	1.3	88	9 AA807361	AA807361 oF50402.8
C	36	25	1.3	90	9 AI348898	AI348898 ta98e03.x
C	37	25	1.3	95	28 AZ801340	AZ801340 2M0059G14
C	38	25	1.3	96	9 AV672532	AV672532 AV672532
C	39	25	1.3	96	29 AG024431	AG024431 Oryza sat
C	40	25	1.3	98	14 CA995243	CA995243 t926d12.Y
C	41	24.8	1.3	79	9 AU007905	AU007905 AU007905
C	42	24.8	1.3	88	9 AI344952	AI344952 tb01c10.x
C	43	24.8	1.3	90	9 AU268769	AU268769 AU268769
C	44	24.8	1.3	91	9 AI251961	AI251961 qv57b12.x
C	45	24.8	1.3	94	9 AI270794	AI270794 qw51a11.x

ALIGNMENTS

RESULT 1
AI349643/c
LOCUS
ta75h07.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2049949 3',
DEFINITION
mRNA sequence.
ACCESSION
AI349643
VERSION
AI349643.1 GI:4086849
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 95)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbsr@mail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

Insert Length: 131   Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .95
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2049949"
/tissue_type="stem cell 34+/38+"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_HSC2"
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from
bone marrow, stem cells 34+/38+, cDNA made by oligo-dr
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 400 bp. Primary library,
non-amplified."
BASE COUNT      73 a      4 c      14 g      4 t
ORIGIN

Query Match      1.6%; Score 29.6; DB 9; Length 95;
Best Local Similarity 57.6%; Pred. No. 5.9e+04;
Matches 53; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1592 GCTACAACTCTATCAGTTTGTGTTTAATGCTTTTATAGCGGCTCTCTGCTTTAAT 1651
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 93 GATACGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTATCCTTTTTTTTTTTTTTTT 34

QY 1652 TTTGCATTTATTGACCATAGGGAATCTTCT 1683
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 TTTTTTTTTTTTTTCCCTTCTGTCGCTTCT 2

RESULT 2
BZ378901
LOCUS      BZ378901              97 bp      DNA      linear      GSS      26-NOV-2002
DEFINITION SALK_112113.42.20.x Arabidopsis thaliana TDNA insertion lines
          Arabidopsis thaliana genomic clone SALK_112113.42.20.x, genomic
          survey sequence.
ACCESSION  BZ378901
VERSION    BZ378901.1 GI:25470183
KEYWORDS   Arabidopsis thaliana (thale cress)
SOURCE     Arabidopsis thaliana
           Arabidopsis thaliana
           Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids
           ; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE  1 (bases 1 to 97)
AUTHORS   Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
           ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
           Zimmerman,J. and Ecker,J.R.
TITLE     A Sequence-Indexed Library of Insertion Mutations in the
          Arabidopsis Genome
JOURNAL    Unpublished
COMMENT    Contact: Joseph R. Ecker
          Salk Institute Genomic Analysis Laboratory (SIGnAL)
          The Salk Institute for Biological Studies
          10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
          Tel: 858 453 4100 x1752
          Email: ecker@salk.edu
          Fax: 858 558 6379
          This is single pass sequence recovered from the left border of
          TDNA.
          Class: TDNA tagged.
          Location/Qualifiers
          1. .97
          /organism="Arabidopsis thaliana"
          /mol_type="genomic DNA"
          /strain="Columbia 0"
          /db_xref="taxon:3702"
          /clone="SALK_112113.42.20.x"
          /clone_lib="Arabidopsis thaliana TDNA insertion lines"
          /note="PCR was performed on Arabidopsis thaliana lines"

```


Directional larval cDNA library originate from Dr.M.Branno, Stazione A.Dohn, Naples, Italy, and was prepared in pBluescript2SK+.

FEATURES
source 1. .99 Location/Qualifiers

/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="019ZE09"
/clone_lib="directional larval cDNA library"
/notes="Vector: pBluescript2SK+"
44 a 5 c 10 g 39 t 1 others

BASE COUNT
ORIGIN

Query Match 1.5%; Score 27.2; DB 9; Length 99;
Best Local Similarity 71.4%; Pred. No. 2e+05;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1730 ATGGTCGGTAAGCAAAATCGCTCAAAATAAGTACCGTTAAACTTAATCT 1778
Db 45 ATTTCCTGTAAGAAATTAGATAAATTAGTAAAGTTAAGTTAAATNT 93

RESULT 7

AW733398

LOCUS sk73a03.y1 Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl016-9701 5', mRNA sequence.

ACCESSION AW733398

VERSION AW733398.1

KEYWORDS GI:7639068

SOURCE EST.

ORGANISM Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 91)

AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,Y., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project

TITLE Unpublished

JOURNAL Contact: Shoemaker R/Public Soybean EST Project

COMMENT Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63109, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cuu@resgen.com

Insert Length: 747 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 85.

FEATURES

source 1. .91

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl016-9701"

/tissue="immature flowers of field grown plants"

/lab_host="Xl10-Gold"

/clone_lib="Gm-cl016"

/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was

6 synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

BASE COUNT 16 a 15 c 24 g 36 t
ORIGIN

Query Match 1.4%; Score 26.6; DB 9; Length 91;

Best Local Similarity 60.3%; Pred. No. 2.6e+05;

Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 617 GCACCTCTTTCTTCTCTAGATACAGGCTATTAAAGGTTTGCCTTGACATGATTTTA 676

Db 18 GGGTGTCTTGTCTCTACCGCTGATTTATTGACGGATCGCTTTTCAACGATTTAA 77

QY 677 GGAATTTTCTCTT 689

Db 78 GGTCTTTTCTTTT 90

RESULT 8

AU061738/c

LOCUS AU061738

DEFINITION AU061738 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium

discoideum cDNA clone SLF614, mRNA sequence.

ACCESSION AU061738

VERSION AU061738.1

KEYWORDS GI:4882842

SOURCE EST.

ORGANISM Dictyostelium discoideum

Dictyostelium discoideum

Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

REFERENCE 1 (bases 1 to 97)

AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,

Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,

Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

Developmental cDNA in Dictyostelium discoideum

Unpublished

Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

Tel: 81-298-53-4664

Fax: 81-298-53-6614

Email: hideko@biol.tsukuba.ac.jp

PROJECT = Dictyostelium discoideum cDNA project in Japan.

FEATURES

source 1. .97

/organism="Dictyostelium discoideum"

/mol_type="mRNA"

/strains="AX4"

/db_xref="taxon:44689"

/clone="SLF614"

/dev_stage="slug"

/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"

BASE COUNT 48 a 7 c 6 g 35 t

ORIGIN

Query Match 1.4%; Score 26.6; DB 9; Length 97;

Best Local Similarity 59.5%; Pred. No. 2.7e+05;

Matches 44; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 647 ATTAAGGGTTTGCCTTGACATGATTTTAGGAATTTTCTCTTCAATGTTACGGCTCTT 706

Db 91 ATTACTAGTTTGTGTACAAATTGATTTACAAANTTAATTTTAACTTTTAAATGTA 32

QY 707 TTCATGACTAAAT 720

Db 31 TTGATATTAAATTT 18

```

FEATURES
  source
    Seq primer: T7.
    Location/Qualifiers
      1..100
        /organism="Vitis vinifera"
        /mol_type="mRNA"
        /culturVar="Shiraz"
        /db_xref="taxon:29760"
        /clone="RB004A06"
        /dev_stage="ripening stage"
        /clone_lib="ripening Grape berries Lambda Zap II Library"
        /notes="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco RI
in Generation of ESTs from Grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier.N.,
Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158
(12): 1575-83 2001"
BASE COUNT      20 a  13 c      59 t
ORIGIN
Query Match      1.4%; Score 26.6; DB 13; Length 100;
Best Local Similarity 60.3%; Pred.No. 2.7e+05;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps' 0;

QY      495  TATTCGAAGAATCCGAGAGGATTTTATTGCTCAAGTCTTAAAAAATCTGTAGAAA 554
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db       80  TATTTTAAATCAATGAAGTTGCAATTATATGGTCTCAAAAAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY      555  AAGGATATACCA 567
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db       20  AAAAAA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 11
AZ781137
LOCUS      AZ781137               76 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION      ZM0019C09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC2M0019C09 F, genomic survey sequence.
ACCESSION      AZ781137
VERSION        AZ781137.1
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
REFERENCE      1 (bases 1 to 76)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
               ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
               and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL         Unpublished
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: rdunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0019 row: C column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 76.
Location/Qualifiers
  1..76
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0019C09"
    /sex="Male"
  
```

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGCIM library"
 /notes="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GII4732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 22 a 10 c 14 g 30 t
 ORIGIN
 Query Match 1.4%; Score 26.4; DB 28; Length 76;
 Best Local Similarity 59.2%; Pred. No. 2.8e+05;
 Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 702 CTCCTTTCATGACTAAATTTTCTTCATGCTGGAGTAAGACCCACATACAGT 761
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 CTCCTTATTTTATTTTCTTCTAGCTGGAGATGATGAACAGAAT 60
 QY 762 TGCATATGATGAATAA 777
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 CCAAGTAACCTGATTA 76

RESULT 12
 AI769234
 LOCUS
 DEFINITION
 wg35e05.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:2367104 3', mRNA sequence.
 AI769234
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 99)
 REFERENCE
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS
 TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 COMMENT
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 1723 Std Error: 0.00
 Seq primer: -400P from Gbco
 High quality sequence stop: 85.
 Location/Qualifiers

1. .99
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2367104"
 /lab host="DH10B"
 /clone lib="Soares NSF_F8_9W_OT_PA_P_S1"
 /notes="Organ: pooled; Vector: pWT3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.

FEATURES
 source

Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and clones: Soares NbHSP pool 1:
 309384-310919, 323208-325895 Soares NbZHP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares Nb2HF8-9W pool 1:
 758280-760583, 772104-774407 Soares NbHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 27 a 10 c 9 g 53 t
 ORIGIN
 Query Match 1.4%; Score 26.2; DB 9; Length 99;
 Best Local Similarity 58.2%; Pred. No. 3.2e+05;
 Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 621 TTCTTTTCTCTAGATACAGGCGCTATTAAAGGTTTCTTTGACATTGATTTAGGAA 680
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 7 TTTTCTTTTACTTTCTAAGGGGAATTTTATCAATATACTTTTACGTTATCAATCT 66
 QY 681 TTTTCTCTTCAATGTTTAC 699
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 67 TTTACAATTTCTAAGTTTTC 85

RESULT 13
 AA647052/c
 LOCUS
 DEFINITION
 vn39ali.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1023548 5', similar to gb:K02109 Mouse 3T3-L1 lipid binding
 protein mRNA, complete cds (MOUSE);, mRNA sequence.
 AA647052
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 80)
 REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

AA647052. 80 bp mRNA linear EST 28-OCT-1997
 vn39ali.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1023548 5', similar to gb:K02109 Mouse 3T3-L1 lipid binding
 protein mRNA, complete cds (MOUSE);, mRNA sequence.
 AA647052
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 80)
 REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

AA647052. 80 bp mRNA linear EST 28-OCT-1997
 vn39ali.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1023548 5', similar to gb:K02109 Mouse 3T3-L1 lipid binding
 protein mRNA, complete cds (MOUSE);, mRNA sequence.
 AA647052
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 80)
 REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

AA647052. 80 bp mRNA linear EST 28-OCT-1997
 vn39ali.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1023548 5', similar to gb:K02109 Mouse 3T3-L1 lipid binding
 protein mRNA, complete cds (MOUSE);, mRNA sequence.
 AA647052
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 80)
 REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

AA647052. 80 bp mRNA linear EST 28-OCT-1997
 vn39ali.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1023548 5', similar to gb:K02109 Mouse 3T3-L1 lipid binding
 protein mRNA, complete cds (MOUSE);, mRNA sequence.
 AA647052
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 80)
 REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.


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Query Match      1.4%; Score 25.6; DB 28; Length 76;
Best Local Similarity 70.8%; Pred. No. 4.2e+05;
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1625 TTTATAGCGGCTCTCTGCTTTAAATTTTGCATTATTATGACCATA 1672
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 TTTATAGCAATCTACTATGATGATGATTTATTTATTTTGGACCAA 68

RESULT 21
BU879460
LOCUS
DEFINITION
V060804 Populus flower cDNA library Populus balsamifera subsp.
trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION
BU879460
VERSION
BU879460.1 GI:24070984
KEYWORDS
EST.
SOURCE
Populus balsamifera subsp. trichocarpa
ORGANISM
Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
1 (bases 1 to 78)
Unneberg,P., Bhalarao,R.R., Jansson,S. and Sterky,F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
JOURNAL
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalarao@plantphys.umu.se.
FEATURES
source
1..78
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/clone_lib="Populus flower cDNA library"
/notes="Organ: flower"
BASE COUNT 30 a 9 c 14 g 25 t
ORIGIN
Query Match      1.4%; Score 25.6; DB 13; Length 78;
Best Local Similarity 59.7%; Pred. No. 4.2e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 762 TGCATATGATGAATAAGTCGTGGGATAAAGCATGATTTCTTGAGAGGATGCACAAAAC 821
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TGTCTTTAGTGAGTATAACGAACACTAATAAGTGAATTTAGAGAGAAAGTAACAAA 61

QY 822 TTTGGGCTGTTT 833
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 TTCCAGCTTCTT 73

RESULT 22
AZ309857
LOCUS
DEFINITION
1M0017M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0017M12 F, genomic survey sequence.
ACCESSION
AZ309857
VERSION
AZ309857.1 GI:10351268
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 87)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
JOURNAL
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: M column: 12
Seq primer: CGTTGTAACACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 87.
Location/Qualifiers
1..87
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 17 a 8 c 20 g 42 t
ORIGIN
Query Match      1.4%; Score 25.6; DB 28; Length 87;
Best Local Similarity 59.7%; Pred. No. 4.3e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 674 TTAGGAATTTCTCTCAATGTTTACGGCTCTTTTCATGACTAAATTTTCTTCATCGTG 733
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 TTGTGTGTGTTAAATGAATTTTACTTTTCAATTTATGTTGATGGGCTCTTGTCTATG 60

QY 734 TCGATGAATAAG 745
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TGTATGTATATG 72

RESULT 23
BH810836
LOCUS
DEFINITION
SALK 051270 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_051270, genomic survey sequence.
ACCESSION
BH810836
VERSION
BH810836.1 GI:20388654
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

```


Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 89)
euroids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab
C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

JOURNAL

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g37610.
Class: TDNA tagged.

FEATURES

source

1..89

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK 051270"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT

ORIGIN

29 a 4 c 16 g 33 t 7 others

Query Match

Best Local Similarity 1.4%; Score 25.6; DB 28; Length 89;

Matches 43; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY

1737 GTAAGAAATCGCTCAAAATAGTACCGTTAACTTAATCTAACGTGTAGCAATATAA 1796

Db

5 GTAAAGAAATGTTGAAGATTGTTATATAATCTTAATTAATCTGTANATGACAAATTTAA 64

QY

1797 AATCTCTTTGGACTTTA 1815

Db

65 AAGNTCTTTTGAANTTA 83

RESULT 24

BI692389/c

LOCUS

603342884F1 NCI_CGAP_Mam2 94 bp mRNA linear EST 18-SEP-2001

DEFINITION

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 94)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA library Preparation: Life Technologies, Inc.

CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11943 row: 9 column: 22

High quality sequence start: 8

High quality sequence stop: 93.

Location/Qualifiers

1..94

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N-3"

/db_xref="taxon:10090"

/clone="IMAGE:5370669"

/tissue_type="tumor, biopsy sample"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam2"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt;

Site: 2; Note: Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH

BASE COUNT

ORIGIN

56 a 3 c 7 g 28 t

Query Match

Best Local Similarity 1.4%; Score 25.6; DB 12; Length 94;

Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY

668 TTGATTTAGGAATTTCTCTCAATGTTTACGGCTCTTTTCATGACTAAATTTTCTTC 727

Db

88° TTTTCTTTTGCATTAATCTCCATATTTTATTTTATTTTACACATTAAATTATTA 29

QY

728 ATGCTGTGGATGAATAAGAC 747

Db

28 ATTTTGTATATATTATAC 9

RESULT 25

BH850307/c

LOCUS

DEFINITION

95 bp DNA linear GSS 13-JUN-2002

SALK 071085.29.45 x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_071085.29.45.x, genomic

survey sequence.

BH850307

BH850307.1 GI:21421178

GSS.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; euroids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 95)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab

C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..95

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

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/clone="SALK_071085.29.45.x"
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/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      29 a   16 c   10 g   40 t
ORIGIN
Query Match      1.4%; Score 25.6; DB 28; Length 95;
Best Local Similarity 55.7%; Pred. No. 4.4e+05;
Matches 49; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 480 ATGCAATGTTCTTATTCGAAAGAAATCCGAGAGAAATTTTATTTGTTCTCAAGTCTTA 539
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 ATTCGAGTAGTTATGATTTTGATAAAAGAAAGAGCTGTTGTTCCCTCATGATCCT 35

QY 540 AAAAATCTGAGAAAGGATATACCAA 567
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 34 AAAATGTCATAAAATGAAAAGGCAA 7

RESULT 26
BX298804
LOCUS
DEFINITION
BX298804 AGENAE Rainbow trout multi-tissues subtracted library
(tcay) Oncorhynchus mykiss cDNA clone tcay0004b.o.06 3prim, mRNA
sequence.
ACCESSION
BX298804
VERSION
BX298804.1 GI:29579449
KEYWORDS
SOURCE
Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE
1 (bases 1 to 100)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0004 row: o column: 6
Seq primer: M13R.
FEATURES
Source
1..100
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcay0004b.o.06"
/tissue type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone lib="AGENAE Rainbow trout multi-tissues subtracted
library (tcay)"
/notes="vector: pT73D-pac; Clone distribution : AGENAE
Resource Centre: Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE"
BASE COUNT      45 a   7 c   23 g   25 t

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```

ORIGIN
Query Match      1.4%; Score 25.6; DB 13; Length 100;
Best Local Similarity 66.1%; Pred. No. 4.4e+05;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 490 TCTTTTATTCGAAGAATCCGAGAGAAATTTTATTTGTTCTCAAGTCTTAAAAAAT 545
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Db 1 TCAAGTACAGGAAGAACATGACAGGTATGTGAGTTGTATAAAATGTTTAAAAAAT 56

RESULT 27
AU013607/c
LOCUS
DEFINITION
AU013607 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc03401, mRNA sequence.
ACCESSION
AU013607
VERSION
AU013607.1 GI:3368398
KEYWORDS
SOURCE
Schizosaccharomyces pombe (fission yeast)
ORGANISM
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE
1 (bases 1 to 81)
Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe
Unpublished
Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1..81
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/db_xref="taxon:4896"
/strain="972"
/clone="spc08401"
/sex="h minus"
/notes="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
BASE COUNT      30 a   11 c   9 g   31 t
ORIGIN
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Best Local Similarity 58.7%; Pred. No. 4.7e+05;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 703 TCTTTTCATGACTAAATTTTCTTCATGCTGTGGATGATTAAGACCCACATACAGTT 762
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Db 80 TTTTATCATGTTAAATTTTATTGATAAAATCGTTATGAPCAAGACGTAAAAAATCCCGT 21

QY 763 GCATATGATGATAAA 777
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 TCATATGATGATAAA 6

RESULT 28
AZ789636/c
LOCUS
DEFINITION
AZ789636 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0037C09 R, genomic survey sequence.
ACCESSION
AZ789636
VERSION
AZ789636.1 GI:12930665
KEYWORDS
GSS.

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SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 70)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 Row: C Column: 09
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 70.
FEATURES
Location/Qualifiers
1..70
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1[4732114]gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 20 a 25 c 15 g
ORIGIN
Query Match 1.4%; Score 25.2; DB 28; Length 70;
Best Local Similarity 62.9%; Pred. No. 5.1e+05;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 625 TTCTCTCTAGATACAGGCGCTATTAAAGGTTTGCTTTGACATTCATTTAGGAATTTT 684
DB 64 TTCCCGCTTGAAGTGCAGTCCCGGCTTGGCTCTGATGGTATTTTGGATAGTGG 5
QY 685 CT 686
DB 4 CT 3
CA330429 79 bp mRNA linear EST 04-NOV-2002

DEFINITION
haa98e07.y1 Fugu hgmpJ adult kidney Takifugu rubripes cDNA clone
6362197.5', mRNA sequence.
ACCESSION
CA330429
VERSION
CA330429.1 GI:24548527
KEYWORDS
EST:
Takifugu rubripes (Fugu rubripes)
SOURCE
Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.
REFERENCE
1 (bases 1 to 79)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy,
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood,
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
AUTHORS
WashU Zebrafish EST Project 1998
TITLE
Unpublished
JOURNAL
Unpublished
COMMENT
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library materials and construction by Greg Elgar (UK MRC HGMP-RC).
DNA Sequencing by: Washington University Genome Sequencing Center
Found through: Fugu clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Putative full length read
The vector to vector length is 80
Seq primer: T3 ET from Amersham.
FEATURES
Location/Qualifiers
1..79
/organism="Takifugu rubripes"
/mol_type="mRNA"
/db_xref="taxon:31033"
/clone="6362197"
/dev_stage="adult"
/lab_host="DH10B (T1-resistant)"
/clone_lib="Fugu hgmpJ adult kidney"
/note="Organ: kidney; Vector: pBluescript II KS
(Stratagene); Site 1: XhoI; Site 2: EcoRI; Library is
oligo-dT primed and directionally cloned using cDNA
prepared with the Stratagene cDNA synthesis kit. Tissue
source: adult kidney. Library materials and construction
by Greg Elgar (UK MRC HGMP-RC)."
BASE COUNT 30 a 12 c 12 g 25 t
ORIGIN
Query Match 1.4%; Score 25.2; DB 14; Length 79;
Best Local Similarity 60.0%; Pred. No. 5.2e+05;
Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 486 ATGTTCTTGTATTCGAAGATCCGAGAGGATTTTATTTGTCCTCAAGTCTTAAARAT 545
DB 10 ATCTCTCTGCTTTTGTAATAATATCTGTGAATAAATATTTTGTCTCAGCGGTTAAAAA 69
QY 546 CTGTAGAAAA 555
DB 70 AAAAAAAAAA 79
RESULT 30
BF102955/c
LOCUS
DEFINITION
601646972F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4073344 5',
mRNA sequence.
ACCESSION
BF102955
VERSION
BF102955.1 GI:10885481
KEYWORDS
EST.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 171 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source Location/Qualifiers
1..90
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2052124"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu26"
/notes="Organ: lung; Vector: pAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 66 a 4 c 14 g 6 t
ORIGIN

Query Match 1.3%; Score 25; DB 9; Length 90;
Best Local Similarity 55.1%; Pred. No. 5.8e+05;
Matches 49; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1595 ACAACTCATCAGTTTGTAAAGCTTTGTTATAGGCGCTCTGCTTAATTTT 1654
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 ACATCATACAGCTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 31
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1655 GCATTATTATGACCATGGATTCTTCT 1683
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 TTTTCTTTTACCCCTCTGCTCTTCT 2
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RECORD 37
AZ801340/C
LOCUS AZ801340
DEFINITION 2M0059G14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0059G14 R, genomic survey sequence.
ACCESSION AZ801340
VERSION AZ801340.1 GI:12953663
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 95)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS Islami,H., Longacre,S., Mahmoud,M., Meener,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00

Plate: 0059 row: G column: 14
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 95.

FEATURES

Location/Qualifiers

1..95

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="JUGC2M0059G14"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 24 a 11 c 32 g 28 t

ORIGIN

Query Match 1.3%; Score 25; DB 28; Length 95;

Best Local Similarity 64.9%; Pred. No. 5.9e+05;
 Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 143 GCACGTCTCAGGGAATTTACCCACCGTAGTGCAGCAACTCCCTCCAGATTTA 199

DB 58 GCAAGCCTCAGAGATATACCAACTTAAGTAGGCACCTCCCTCATATTAA 2

RESULT 38

AV672532

LOCUS

DEFINITION AV672532 Nori Satoh unpublished cDNA library Ciona intestinalis

cdna clone citb512 5', mRNA sequence.

ACCESSION AV672532.1 GI:10110531

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 96)

AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL Unpublished

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..96

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

FEATURES

source

/clone="citb512"

/tissue type="whole animal"

/dev_stage="tailbud"

/clone_lib="Nori Satoh unpublished cDNA library"

BASE COUNT 39 a 5 c 12 g 40 t

ORIGIN

Query Match 1.3%; Score 25; DB 9; Length 96;

Best Local Similarity 69.4%; Pred. No. 5.9e+05;
 Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1730 ATGTCCTGAAGAAATCGTCAAAATAGTACCGTTAAACTTAATCT 1778

DB 13 ATTTCTCTGGAAGAAATAGATGAATTAAGTAAAGTTAAGTTAAATGT 61

RESULT 39

AG024431

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) DNA, clone:ND4563.0.101.1A, 3' flanking sequence of Tos17 insertion in rice strain ND4563, genomic survey sequence.

ACCESSION AG024431 GI:7683095

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1

AUTHORS Miyao,A. and Hirochika,H.

TITLE Rice insertion mutants

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 96)

AUTHORS Miyao,A., Tanaka,K. and Hirochika,H.

TITLE Direct Submission

JOURNAL Submitted (25-OCT-1999) Akio Miyao, National Institute of

Agricultural Sciences, Molecular Genetics; 2-1-2, Kannondai,
 Tsukuba, Ibaraki 305-8602, Japan [E-mail:miyao@affrc.go.jp,
 URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
 Fax:81-298-38-7020]

FEATURES

Location/Qualifiers

1..96

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/strain="ND4563"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="ND4563.0.101.1A"

/clone_lib="PCR product directly amplified from rice

genomic DNA"

/note="The 3' end of retrotransposon Tos17 was found

immediately upstream of this sequence."

BASE COUNT 26 a 17 c 14 g 37 t

ORIGIN

Query Match 1.3%; Score 25; DB 29; Length 96;

Best Local Similarity 58.9%; Pred. No. 5.9e+05;
 Matches 43; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 327 TGATGAGCGTATATTATAGATTGGAGCGTCATCTTCGGGAGCTGTTCTTCTGAATC 386

DB 1 TGATCATAGTATGTACGAACCTTGGATCAACGATCATCAAAATTTGCTAATTCATA 60

QY 387 TTTTGTCTTATCTG 399

DB 61 TTTTGTCTTCTG 73

RESULT 40

CA995243

LOCUS

CA995243 98 bp mRNA linear EST 07-JAN-2003

```

DEFINITION   rg26b12.v1 Meloidogyne hapla J2 SL1 TOPO v1 Meloidogyne hapla cDNA
              5', mRNA sequence.
ACCESSION    CA995243
VERSION      CA995243.1 GI:27540114
KEYWORDS     EST.
SOURCE       Meloidogyne hapla
ORGANISM     Meloidogyne hapla
              Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
              Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE    1 (bases 1 to 98)
AUTHORS      McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,
              Dante, M., Maier, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
              Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarishvili, R.,
              Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
              M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,
              Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
              Wilson, R.
TITLE        The Washington Univ. Nematode EST Project, 1999
JOURNAL      Unpublished
COMMENT      Contact: McCarter JP
              The Washington Univ. Nematode EST Project, 1999
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              The library was constructed by Claire Murphy and Dr. James McCarter
              at Washington University, St. Louis. J2 were provided by Dr.
              Valerie Williamson of the University of California at Davis
              (vmwilliamson@ucdavis.edu).
              Putative full length read
              The vector to vector length is 99
              Seq primer: -40RP from Gibco.
              Location/Qualifiers
              1..98
              /organism="Meloidogyne hapla"
              /mol_type="mRNA"
              /db_xref="taxon:6305"
              /seq_version="J2"
              /lab_host="DH10B"
              /clone_lib="Meloidogyne hapla J2 SL1 TOPO v1"
              /notes="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
              Site 2: EcoRI; The library was constructed by Claire
              Murphy and Dr. James McCarter at Washington University,
              St. Louis. Oligo(dT)-SL1 PCR based library. Meloidogyne
              hapla J2 cDNA PCR products of size >400 nucleotides
              containing SL1 on the 5' end and oligo(dT) on the 3' end
              were non-directionally cloned into pCRII-TOPO(Invitrogen)
              following the TOPO TA cloning protocol. J2 were provided
              by Dr. Valerie Williamson of University of California at
              Davis (vmwilliamson@ucdavis.edu)."
              41 a 11 c 9 g 37 t
              BASE COUNT 41 a 11 c 9 g 37 t
              ORIGIN
              Query Match 1.3%; Score 25; DB 14; Length 98;
              Best Local Similarity 55.1%; Pred. No. 5.9e+05;
              Matches 49; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1385 TTTATAGCACATTCCTTTTGAAGAAATTCAAATAGATTGCAAGCCATTGGTGCTTTA 1444
Db 7 TATATAACTAATCGTTGGTTGTTATTTAAATTAATAAATAATTTCTTCAATGGCTATATCA 66
QY 1445 ATGACTGTATGGGGTATTCATTAAACAA 1473
Db 67 ATTTGTACATTAAAGTGAACCTTTAAAAA 95

RESULT 41
LOCUS       AU007905/c
DEFINITION Schizosaccharomyces pombe late log phase cDNA
              Schizosaccharomyces pombe cDNA clone spc02639, mRNA sequence.
ACCESSION   AU007905
VERSION      AU007905.1
KEYWORDS     EST.
SOURCE       Schizosaccharomyces pombe
ORGANISM     Schizosaccharomyces pombe
              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
              Schizosaccharomycetales; Schizosaccharomycetaceae;
              1 (bases 1 to 79)
              Morimyo, M. and Mita, K.
              Identification of expressed sequence tags of Schizosaccharomyces
              pombe
              Unpublished
              Contact: Mitsuo Morimyo
              Genome Research Group
              National Institute of Radiological Sciences
              9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
              Email: morimyo@nirs.go.jp.
              Location/Qualifiers
              1..79
              /organism="Schizosaccharomyces pombe"
              /mol_type="mRNA"
              /strain="972"
              /db_xref="taxon:4896"
              /clone="spc02639"
              /sex="h minus"
              /note="Vector: M13mp19; The cDNA library of
              Schizosaccharomyces pombe was prepared by cloning cDNA
              into the SmaI site of M13mp19 DNA and the direction of DNA
              sequences was not always from 5' to 3'. The cDNA data of
              Schizosaccharomyces pombe are available for searching on
              the World Wide Web. (URL, http://www.nirs.go.jp)"
              40 a 5 c 13 g 20 t
              BASE COUNT 40 a 5 c 13 g 20 t
              ORIGIN
              Query Match 1.3%; Score 24.8; DB 9; Length 79;
              Best Local Similarity 59.4%; Pred. No. 6.3e+05;
              Matches 41; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1663 TATGACCATAGGATCTCTTAGGAACCTTATCGTCTCTTATATTCACACCTCTGTT 1722
Db 71 TATGCTATGTTCTTTTAAACAGTACTTTTAACTTTGTTTATCTTGTTCATTATT 12
QY 1723 GTTGTTTAT 1731
Db 11 CTAATTAT 3

RESULT 42
LOCUS       AU007905/c
DEFINITION Homo sapiens
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 88)
              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-rc@mail.nih.gov
              CDNA Library Preparation: David B. Krizman, Ph.D.
              CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              www-bio.lnl.gov/bbrp/image/image.html

```


QY 1406 AGAAAAATTCAAATAGATTTCGAAGCCATTGGTGGCTTTTAATGACTGCTATTGGGTATTCA 1466
 Db 85 AAAAAAAAAAAAAAAAAATAAAAAATCGTTTTTGTGTTTAAACAGGGTAATTATATATTG 26
 QY 1466 TTAACAACAATCTTTGATCATTTT 1489
 Db 25 ATCAACAATAATTTTAATTTTTT 2

AI251961 91 bp mRNA linear EST 02-DEC-1998
 QV57B12.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985663 3',
 mRNA sequence.
 ACCESSION AI251961
 VERSION AI251961
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 91)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 unknown library type
 Insert Length: 169 Std Error: 0.00
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1..91
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1985663"
 /sex="female"
 /issue_type="papillary serous carcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ov32"
 /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.
 Non-directionally cloned. Size-selected on agarose gel,
 average insert size 500 bp. Non-amplified library."
 70 a 6 c 12 g 3 t

BASE COUNT 70 a 6 c 12 g 3 t
 ORIGIN

Query Match 1.3%; Score 24.8; DB 9; Length 91;
 Best Local Similarity 57.9%; Pred. No. 6.4e+05;
 Matches 44; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1608 TTTTGTAAATGCTTTTGTATTATAGCGGCTCTCTCTCTTTAAATTTGCATTTATTATGA 1667
 Db 77 TTTTGTAAATGCTTTTGTATTATAGCGGCTCTCTCTCTTTAAATTTGCATTTATTATGA 1667
 QY 1668 CNAATAGGATTCCTCT 1683
 Db 17 CCTCTGTCGCTCTCT 2

RESULT 45
 AI270794/c
 LOCUS AI270794
 DEFINITION QW51a11.x1 NCI_CGAP_Br13 Homo sapiens cDNA clone IMAGE:1994588 3',
 mRNA sequence.
 ACCESSION AI270794
 VERSION AI270794
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 94)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbsr@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..94
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1994588"
/sex="female"
/tissue_type="breast carcinoma in situ"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Br13"
/notes="Organ: breast; Vector: pAMP1; mRNA made from breast
carcinoma, cDNA made by oligo-dr priming. Directionally
cloned. Size-selected on agarose gel, average insert
size 500 bp. Primary library, non-amplified."
65 a 6 c 19 g 4 t
BASE COUNT
ORIGIN
Query Match 1.3%; Score 24.8; DB 9; Length 94;
Best Local Similarity 54.3%; Pred. No. 6.5e+05;
Matches 50; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 1592 GCTACACTATACGTTTGTAAATGCTTTGTTTATAGGGGCTCCTCTCTTAAAT 1651
Db 93 GATACGACATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTCTTATC 34
QY 1652 TTTCATTATTATGACCATAGGATCTTCT 1683
Db 33 TTTCCTTTTGTCCCTCTCTCTCTCT 2
Search completed: October 23, 2003, 09:20:09
Job time : 3604 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 09:20:14 ; Search time 3602 Seconds
(without alignments)
12577.330 Million cell updates/sec

Title: US-09-868-987-1
Perfect score: 1864
Sequence: 1 atggacttcgcattgtgc.....atgacaatttcagataatgc 1864

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 71794

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vt:*
- 21: em_gss_fun:*
- 22: em_gss_man:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22.4	1.2	36	28	BH907371
2	19.4	1.0	34	9	AI041455
3	19.4	1.0	39	28	AZ779322
4	19.4	1.0	40	9	AI318679

C	5	19.2	1.0	40	9	AA068300
C	6	18.8	1.0	35	28	AZ785768
C	7	18.8	1.0	40	9	AU264483
C	8	18.6	1.0	38	29	BZ761950
C	9	18.4	1.0	39	12	BZ057535
C	10	18.2	1.0	35	29	BZ358798
C	11	18.2	1.0	39	14	CO1981
C	12	18.2	1.0	40	9	AI022013
C	13	18	1.0	37	9	AL849593
C	14	18	1.0	39	9	AU266702
C	15	18	1.0	39	9	AV853005
C	16	18	1.0	39	29	BZ761743
C	17	17.8	1.0	36	28	AZ647867
C	18	17.8	1.0	37	28	AZ448035
C	19	17.8	1.0	38	14	H57900
C	20	17.8	1.0	38	28	BH864598
C	21	17.8	1.0	39	28	AG227568
C	22	17.8	1.0	40	28	AZ767521
C	23	17.6	0.9	34	9	AU259110
C	24	17.6	0.9	34	29	AG218655
C	25	17.6	0.9	35	29	BZ763041
C	26	17.6	0.9	37	29	BZ768062
C	27	17.6	0.9	40	28	BH789828
C	28	17.6	0.9	40	29	BZ663364
C	29	17.4	0.9	28	9	AA863634
C	30	17.4	0.9	35	28	BH866003
C	31	17.4	0.9	38	28	BH864481
C	32	17.4	0.9	39	28	AZ772005
C	33	17.4	0.9	40	28	AZ345478
C	34	17.2	0.9	30	28	BH864835
C	35	17.2	0.9	31	9	AU989540
C	36	17.2	0.9	31	9	AU265359
C	37	17.2	0.9	33	14	CO0007
C	38	17.2	0.9	36	28	AZ481068
C	39	17.2	0.9	38	28	AZ317175
C	40	17.2	0.9	38	28	AZ583903
C	41	17.2	0.9	39	28	CC057135
C	42	17.2	0.9	39	29	AL752023
C	43	17.2	0.9	40	9	AA116378
C	44	17.2	0.9	40	9	AJ237274
C	45	17.2	0.9	40	12	BI693481

ALIGNMENTS

RESULT 1
BH907371
LOCUS
DEFINITION
BH907371.1 GI:22720304
36 bp DNA linear GSS 04-SEP-2002
SALK_042003.18.65.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_042003.18.65.x, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Brassicales; Brassicaceae; Arabidopsi
REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadtrina
C., Jaeka,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .36
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"

/clone="SALK 042003.18.65.x"
/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
13 t

BASE COUNT 14 a 4 c 5 g
ORIGIN
Query Match 1.2%; Score 22.4; DB 28; Length 36;
Best Local Similarity 81.2%; Pred. No. 1.9e+06;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1027 TATTCACACATTGGATCTTCAGAAAGATCA 1058

Db 5 TATTCACACACTAGTATTTTCAGAGAGATTA 36

RESULT 2

AI041455

LOCUS

DEFINITION
ow36c10.s1 Soares parathyroid tumor NBHPA Homo sapiens cDNA clone
IMAGE:1648914 3' similar to SW:NU4M HUMAN P03905 NADH-UBIQUINONE
OXIDOREDUCTASE CHAIN 4 ; mRNA sequence.

ACCESSION

AI041455

VERSION

AI041455.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 34)

AUTHORS

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 532 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .34

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1648914"

/tissue_type="parathyroid tumor"

/dev_stage="adult"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares parathyroid tumor NBHPA"

/notes="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia

FEATURES

source

) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer.

15'-TGTTACCAATCTGAAGTGGAGCGCGCCACCAATTTTITTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

BASE COUNT 17 a 5 c 8 g 4 t
ORIGIN
Query Match 1.0%; Score 19.4; DB 9; Length 34;
Best Local Similarity 79.3%; Pred. No. 8.2e+06;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 541 AAAATCTGTAGAAAAGGATATACCAAGG 569

Db 1 AAAATATGCCCAAAAGGATATACCAAGG 29

RESULT 3

AZ779322

LOCUS

DEFINITION

2M0015A11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0015A11 R, genomic survey sequence.

ACCESSION

AZ779322

VERSION

AZ779322.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 39)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: A column: 11
Seq primer: CACACAGGAACACAGCTATCACC
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
1. .39
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0015A11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 1.0%; Score 19.4; DB 28; Length 39;
Best Local Similarity 70.3%; Pred. No. 8.3e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 296 GCATGCTGGCTGGCAATGCTTATGTTTCATGA 332
|||||
Db 1 GCTTGCTTCCATACCAATACTATATTTTGTTA 37
|||||

RESULT 4
LOCUS AI1318679/c
DEFINITION ta49g08.x1 NCI CGAP Lu25 Homo sapiens cDNA clone IMAGE:2047454 3', similar to TR:Q34096 Q34096 MURF2 PROTEIN. ;, mRNA sequence.
ACCESSION AI1318679
VERSION AI1318679.1 GI:4034614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2047454"
/tissue_type="bronchioalveolar carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu25"
/notes="Organ: lung; Vector: pAMP1; mRNA made from lung carcinoma tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

BASE COUNT
ORIGIN

Query Match 1.0%; Score 19.4; DB 28; Length 39;
Best Local Similarity 70.3%; Pred. No. 8.3e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 296 GCATGCTGGCTGGCAATGCTTATGTTTCATGA 332
|||||
Db 1 GCTTGCTTCCATACCAATACTATATTTTGTTA 37
|||||

BASE COUNT
ORIGIN

Query Match 1.0%; Score 19.4; DB 28; Length 39;
Best Local Similarity 70.3%; Pred. No. 8.3e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 296 GCATGCTGGCTGGCAATGCTTATGTTTCATGA 332
|||||
Db 1 GCTTGCTTCCATACCAATACTATATTTTGTTA 37
|||||

Query Match 1.0%; Score 19.4; DB 9; Length 40;
Best Local Similarity 70.3%; Pred. No. 8.4e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1229 AAACATATCGAGAAATCGTTATCAGCGGACCATCG 1265
|||||
Db 40 AAACAAACAAACAAACAAATACATATCAGGTAAACATTTG 4
|||||

RESULT 5
LOCUS AA068300/c
DEFINITION mm61h03.r1 Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:532949 5', similar to TR:G1050752 KYNURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE ;, mRNA sequence.

ACCESSION AA068300
VERSION AA068300.1 GI:1566558
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 40)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:319885

Possible reversed clone: similarity on wrong strand
Seq primer: -28mi3 rev1 ET from Amersham
High quality sequence stop: 13.
Location/Qualifiers
1. 40
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:532949"
/tissue_type="carcinoma"
/dev_stage="embryonic"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse embryonic carcinoma (#937317)"

BASE COUNT
ORIGIN

Query Match 1.0%; Score 19.2; DB 9; Length 40;
Best Local Similarity 75.0%; Pred. No. 9.2e+06;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 921 CCTTTACCTTTTAAATCCAAAGAGCATGCGATC 952
|||||
Db 39 CCTTTACCTTTTAAATCCAAAGAGCATGCGATC 8
|||||

BASE COUNT
ORIGIN

Query Match 1.0%; Score 19.2; DB 9; Length 40;
Best Local Similarity 75.0%; Pred. No. 9.2e+06;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 921 CCTTTACCTTTTAAATCCAAAGAGCATGCGATC 952
|||||
Db 39 CCTTTACCTTTTAAATCCAAAGAGCATGCGATC 8
|||||

RESULT 6
AZ785768/c

LOCUS AZ785768 35 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0030C04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0030C04 F, genomic survey sequence.
 ACCESSION AZ785768
 VERSION GSS.
 KEYWORDS AZ785768.1 GI:112922858
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 35)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Authors Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0030 row: C column: 04
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 35.
 Location/Qualifiers
 1..35
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0030C04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 BASE COUNT 6 a 3 c 7 g 19 t
 ORIGIN
 Query Match 1.0%; Score 18.8; DB 28; Length 35;
 Best Local Similarity 76.7%; Pred. No. 1.1e+07;
 Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 539 AAAAAATCTGTAGAAAAGATATACCAAG 568
 |||||
 Db 30 AAAAAATCTATTGAGACATAAATACCAAG 1
 |||||
 RESULT 7

AU2644483/c
 LOCUS AU264483 40 bp mRNA linear EST 10-MAY-2002
 DEFINITION VS Dictyostelium discoideum CDNA clone VSD733 5', mRNA
 sequence.
 ACCESSION AU264483
 VERSION AU264483.1 GI:20523281
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 1 (bases 1 to 40)
 REFERENCE Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
 Authors Takeuchi,I., Kohara,Y. and Tanaka,Y.
 TITLE Population analysis of cDNAs from unicellular and multicellular
 stages of Dictyostelium discoideum
 JOURNAL Unpublished
 COMMENT Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp.
 Location/Qualifiers
 1..40
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="VSD733"
 /sex="mat A"
 /dev_stage="vegetative"
 /clone_lib="VS"

FEATURES

source
 BASE COUNT 17 a 4 c 0 g 19 t
 ORIGIN
 Query Match 1.0%; Score 18.8; DB 9; Length 40;
 Best Local Similarity 68.4%; Pred. No. 1.1e+07;
 Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 520 TTTATTGCTCAAGCTCTTAAAAATCTGTAGAAAAG 557
 |||||
 Db 40 TTTTITTTTAAAAATGTTTAAAAAAGATTAAAAAG 3
 |||||

RESULT 8

BZ761950
 LOCUS BZ761950 38 bp DNA linear GSS 13-MAR-2003
 DEFINITION SALK 083640.22.00.n Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_083640.22.00.n, genomic
 survey sequence.
 ACCESSION BZ761950
 VERSION BZ761950.1 GI:28934503
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 38)
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..38

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_083640.22.00.n"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 14 a 5 c 3 g 16 t

ORIGIN

Query Match 1.0%; Score 18.6; DB 29; Length 38;

Best Local Similarity 72.7%; Pred. No. 1.2e+07;

Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1381 CTTGTTTATAGCACATTTCTTTTGAGGAAAT 1413

|||||

Db 1 CTTTATTACACATATTTCAATTTGAAGATCAT 33

|||||

RESULT 9

BJ057535 39 bp mRNA linear EST 10-DEC-2001

LOCUS

DEFINITION

laevis cDNA clone XL104fil 5', mRNA sequence.

ACCESSION

BJ057535

VERSION

BJ057535.1 GI:17479605

KEYWORDS

EST.

SOURCE

Xenopus laevis (African clawed frog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.

REFERENCE

1 (bases 1 to 39)

AUTHORS

Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara Y.

TITLE

Expressed genes in X. laevis embryo

JOURNAL

Unpublished

COMMENT

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshin@genes.nig.ac.jp.

FEATURES

source

Location/Qualifiers

1..39

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL104fil"

/tissue_type="whole embryo"

/dev_stage="stage 25"

/clone_lib="NIBB Mochii normalized Xenopus tailbud library"

BASE COUNT 11 a 2 c 4 g 21 t 1 others

ORIGIN

Query Match 1.0%; Score 18.4; DB 12; Length 39;

Best Local Similarity 67.6%; Pred. No. 1.4e+07;

Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 509 CGAGAGGAATTTTATTTGTTCAAGTCTTAAAGAAAT 545

|||||

|||||

Db

RESULT 10

BJ058798/c

LOCUS

DEFINITION

SALK_133323.42.50.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_133323.42.50.x, genomic survey sequence.

ACCESSION

BJ058798

VERSION

BJ058798.1 GI:24951256

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

euroids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

1 (bases 1 to 35)

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 X1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

source

Location/Qualifiers

1..35

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_133323.42.50.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 15 a 5 c 6 g 9 t

ORIGIN

Query Match 1.0%; Score 18.2; DB 29; Length 35;

Best Local Similarity 74.2%; Pred. No. 1.5e+07;

Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1466 TTAAACAATACCTTTCATCATTTTTCATCGTA 1496

|||||

Db 32 TTATCCATATTTTCACCATGTTTGTAGTA 2

|||||

RESULT 11

CO1981/c

LOCUS

DEFINITION

HUMS0003999 Human adult (K.Okubo) Homo sapiens cDNA, mRNA sequence.

ACCESSION

CO1981

VERSION

CO1981.1 GI:1434211

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 39)

AUTHORS TITLE JOURNAL COMMENT

Okubo,K.
BodyMap: human gene expression database
Unpublished
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kouseku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
found there.

FEATURES

source
1. 39
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
BASE COUNT 16 a 2 c 3 g 18 t
ORIGIN
Query Match 1.0%; Score 18.2; DB 14; Length 39;
Best Local Similarity 66.7%; Pred. No. 1.5e+07;
Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1762 ACCGTAAACTTAATCTAGCTAGCAATATAAAATC 1800
DB 39 AACTTAAATATATATCATCTATTGAATATAAGATC 1

RESULT 12

AI022013/c
LOCUS
DEFINITION
OW64c01.x1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA
clone IMAGE:1651584 3' similar to TR:Q35993 Q35993 CYTOCHROME C
OXIDASE III. ; mRNA sequence.
ACCESSION AI022013
VERSION AI022013.1 GI:3239366
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 400 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

source
1. 40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1651584"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts_NBHSF"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V.TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 25 a 10 c 0 g 5 t

ORIGIN

Query Match 1.0%; Score 18.2; DB 9; Length 40;
Best Local Similarity 66.7%; Pred. No. 1.5e+07;
Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 824 TGGCGTGTTCGGAAGTGTTCCTTTTCTTTAGGTGCGTT 862
DB 40 TGTGATTTTATTGTGAGTGATTTTGTTCCTTTAGGTGTT 2

RESULT 13

AL849593/c
LOCUS
DEFINITION
AL849593 XGC-egg Silurana tropicalis cDNA clone TEGg061n22 5', mRNA
sequence.
ACCESSION AL849593.1 GI:22869815
VERSION AL849593
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 37)
Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2002
Unpublished
Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE.ID: TEGg061n22.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.

FEATURES

source
1. 37
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEGg061n22"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
BASE COUNT 15 a 4 c 3 g 15 t
ORIGIN
Query Match 1.0%; Score 18; DB 9; Length 37;
Best Local Similarity 70.6%; Pred. No. 1.7e+07;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1378 AGTCTGTTTATAGCACATTCCTTTTGAAGAAA 1411
DB 34 ACGATTGTTAGATATATCTCTTTTGAAGAAA 1

RESULT 14

AU266702


```

LOCUS       AU266702               39 bp  mRNA  linear  EST 10-MAY-2002
DEFINITION   AU266702 VS Dictyostelium discoideum cDNA clone VSG660 5', mRNA
ACCESSION   AU266702
VERSION     AU266702.1  GI:20525500
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
ORGANISM    Dictyostelium discoideum
REFERENCE   1 (bases 1 to 39)
AUTHORS     Urushihara H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,
            Takeuchi, I., Kohara, Y., and Tanaka, Y.
TITLE       Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
JOURNAL     Unpublished
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.

FEATURES             Location/Qualifiers
     source          1..39
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSG660"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"

BASE COUNT      14 a      0 g      20 t      5 others
ORIGIN
1  TTTCTTTTGAAGAAATTCAAATAGATT 1425
2  TTTCTTTTAAAAAATNAAANNNTTT 30

Query Match      1.0%; Score 18; DB 9; Length 39;
Best Local Similarity 70.0%; Pred. No. 1.7e+07;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY  1396  TTTCTTTTGAAGAAATTCAAATAGATT 1425
DB  1  TTTCTTTTAAAAAATNAAANNNTTT 30

RESULT 15
LOCUS       AV853005               39 bp  mRNA  linear  EST 08-NOV-2001
DEFINITION   AV853005 Nori Satoh unpublished cDNA library, egg Ciona
            intestinalis cDNA clone rcieg16c15 3', mRNA sequence.
ACCESSION   AV853005
VERSION     AV853005.1  GI:16838721
KEYWORDS    EST.
SOURCE      Ciona intestinalis
ORGANISM    Ciona intestinalis
REFERENCE   1 (bases 1 to 39)
AUTHORS     Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
TITLE       Expressed genes in Ciona intestinalis
JOURNAL     Unpublished
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@acidian.zool.kyoto-u.ac.jp.

FEATURES             Location/Qualifiers
     source          1..39
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="rcieg16c15"

```

```

/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

BASE COUNT      13 a      12 c      3 g      10 t      1 others
ORIGIN
1  CGAGCCCTATTTTAAACGTCCTCCATTCGAAATCAT 142
2  GCAACCTATANATAACTTCCCAATGACAACACTT 36

Query Match      1.0%; Score 18; DB 9; Length 39;
Best Local Similarity 68.6%; Pred. No. 1.7e+07;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY  108  CGAGCCCTATTTTAAACGTCCTCCATTCGAAATCAT 142
DB  2  GCAACCTATANATAACTTCCCAATGACAACACTT 36

RESULT 16
LOCUS       BZ761743/c              39 bp  DNA  linear  GSS 13-MAR-2003
DEFINITION   BZ761743 SALK_080903.44.85.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_080903.44.85.x, genomic
            survey sequence.
ACCESSION   BZ761743
VERSION     BZ761743.1  GI:28934296
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (chale cress)
ORGANISM    Arabidopsis thaliana
REFERENCE   1 (bases 1 to 39)
AUTHORS     Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab,
            C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
            Zimmerman, J. and Ecker, J.R.
TITLE       A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL     Unpublished
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.

Class: TDNA tagged
Location/Qualifiers
     source          1..39
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_080903.44.85.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT      20 a      5 c      2 g      12 t

Query Match      1.0%; Score 18; DB 29; Length 39;
Best Local Similarity 70.6%; Pred. No. 1.7e+07;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY  1395  ATTCTTTTGAAGAAATTCAAATAGATTGCA 1428
DB  39  ATTCTTTTATGATATTAATAGATGCGTTCA 6

RESULT 17

```

AZ647867/c
 LOCUS AZ647867 36 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0514B09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0514B09 R, genomic survey sequence.
 ACCESSION AZ647867
 VERSION AZ647867.1 GI:11779762
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0514 row: B column: 09
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 36.
 Location/Qualifiers
 1..36
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0514B09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES source

1..36
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0514B09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 12 a 3 c 6 g 15 t

ORIGIN

Query Match 1.0%; Score 17.8; DB 28; Length 36;
 Best Local Similarity 75.9%; Pred. No. 1.8e+07;
 Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1392 CACATTCCTTTTGAAGAAATTCAAATA 1420
 ||||| |
 DB 30 CACATATAGTTTGAAGAAATTCATTAATA 2

RESULT 18
 AZ448035/c
 LOCUS AZ448035 37 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0245D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0245D02 R, genomic survey sequence.
 ACCESSION AZ448035
 VERSION AZ448035.1 GI:10600427
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0245 row: D column: 02
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 37.
 Location/Qualifiers
 1..37
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0245D02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES source

1..37
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0245D02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 12 a 17 c 0 g 8 t

ORIGIN

Query Match 1.0%; Score 17.8; DB 28; Length 37;
 Best Local Similarity 90.5%; Pred. No. 1.8e+07;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 892*TTTGGATGATTTTAAAGG 912
 |
 DB 28 TGTGGATGATTTTGAAGG 8

```

RESULT 19
H57900
LOCUS
DEFINITION
  yrl4c09.r1 Soares fetal liver spleen INFLS EST 05-OCT-1995
  IMAGE:205264 S' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN
  PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
H57900
VERSION
H57900.1 GI:1010732
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 38)
AUTHORS
  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
  M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
  Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
  R., Williamson,A., Wohldmann,P. and Wilson,R.
  The WashU-Merck EST Project
  Unpublished
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Insert Size: 1120
  High quality sequence starts: 1
  High quality sequence stops: 1
  Source: IMAGE Consortium, LNL
  This clone is available royalty-free through LNL; contact the
  IMAGE Consortium (info@image.lnl.gov) for further information.
  Trace considered overall poor quality
  Insert length: 1120 Std Error: 0.00
  Seq primer: M13RP1
  High quality sequence stop: 1.
  Location/Qualifiers
    1..38
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GB:3780072"
      /db_xref="taxon:9606"
      /clone="IMAGE:205264"
      /sex="male"
      /dev_stage="20 week-post conception fetus"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares fetal liver spleen INFLS"
      /notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
      with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
      1st strand cDNA was primed with a Pac I - oligo(dT) primer
      [5' ACTCGAGAGTAATTAAGATCTTTTCTTTTCTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Pac I and cloned into the Pac I
      and Eco RI sites of the modified pT7T3 vector. Library
      went through one round of normalization. Library
      constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 3 a 5 c 8 g 21 t
ORIGIN
  Query Match 1.0%; Score 17.8; DB 14; Length 38;
  Best Local Similarity 65.8%; Pred. No. 1.8e+07;
  Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1608 TTTTGTATGCTTTTGTATTATAGCGGCTCTCTGTC 1645
      ||||| | ||||| ||||| ||||| |||||
Db 1 TTTTGTATGCTTTTGTATTATAGCGGCTCTCTGTC 38
      ||||| | ||||| ||||| ||||| |||||

RESULT 20
BH864598
LOCUS
DEFINITION
  SALK_096314 Arabidopsis thaliana TDNA insertion lines Arabidopsis
  thaliana genomic clone SALK_096314, genomic survey sequence.
ACCESSION
BH864598
VERSION
BH864598.1 GI:22100496
KEYWORDS
GSS
ORGANISM
Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsais.
REFERENCE
1 (bases 1 to 38)
AUTHORS
  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
  C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
  Zimmerman,J. and Ecker,J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGNAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  TDNA.
  Class: TDNA tagged.
  Location/Qualifiers
    1..38
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /strain="Columbia 0"
      /db_xref="taxon:3702"
      /clone="SALK_096314"
      /clone_lib="Arabidopsis thaliana TDNA insertion lines"
      /note="PCR was performed on Arabidopsis thaliana lines
      each of which contains one or more TDNA insertion
      elements. The resultant fragment for each line was
      directly sequenced to determine the genomic sequence at
      the site of insertion. Details of the protocols used can
      be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 12 a 1 c 10 g 15 t
ORIGIN
  Query Match 1.0%; Score 17.8; DB 28; Length 38;
  Best Local Similarity 67.6%; Pred. No. 1.8e+07;
  Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1789 AATATAAAATCTCTTTGGGACTTTAGTCCCAAGG 1825
      ||||| | ||||| ||||| ||||| |||||
Db 2 ATTTAGAGATCTTTTATGGGATTTAGTGAAAAAGG 38
      ||||| | ||||| ||||| ||||| |||||

RESULT 21
AG227568
LOCUS
DEFINITION
  Lotus japonicus DNA, clone:ljB141114_f, genomic survey sequence.
ACCESSION
AG227568
VERSION
AG227568.1 GI:26538192
KEYWORDS
GSS.
SOURCE
Lotus japonicus
ORGANISM
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
REFERENCE
1
AUTHORS
  Sato,S., Nakamura,Y. and Tabata,S.
  Lotus japonicus BAC End sequences
  Published Only in Database (2002)
  JOURNAL
  2 (bases 1 to 39)
REFERENCE
AUTHORS
  Sato,S.
  Direct Submission
  Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,

```

The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-Kamata-ari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>,
Tel: 81-438-52-3935(ex.2336), Fax: 81-438-52-3934)

FEATURES

Location/Qualifiers
source

1. .39
/organism="Lotus japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
/clone="LjB141114 f"
/clone_lib="genomic BAC library"
/notes="VECTOR:pBelOBAC11"
BASE COUNT 10 a 6 c 5 g 18 t
ORIGIN

Query Match 1.0%; Score 17.8; DB 29; Length 39;
Best Local Similarity 67.6%; Pred. No. 1.8e+07;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1374 GTGCAGCTCTGTTATAGCAATTTCTTTTGAAGAA 1410

Db 3 GTTCACAAATTATGATAACACATTTCTTCTTAGGA 39

RESULT 22

AZ767521

LOCUS AZ767521 40 bp DNA linear GSS 16-FEB-2001
DEFINITION cMO566D18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0566D18 R, genomic survey sequence.

ACCESSION AZ767521

VERSION AZ767521.1 GI:12885699

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
and Wright, D., Weis, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0566 row: D column: 18

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

FEATURES

source

1. .40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0566D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 6 a 5 c 8 g 21 t
ORIGIN

Query Match 1.0%; Score 17.8; DB 28; Length 40;
Best Local Similarity 67.6%; Pred. No. 1.8e+07;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 822 TTTCGGCTCTTCTGGAAGTGTCTTTCTTTAGGTTG 858

Db 2 TCTGCACATAATCTGGAAGTGTCTTTCTTTAGGTTG 38

RESULT 23

AU259110/c

LOCUS AU259110 34 bp mRNA linear EST 25-APR-2002

DEFINITION AU259110 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0014559 3', mRNA sequence.

ACCESSION AU259110

VERSION AU259110.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 34)

AUTHORS Kato, K. and Matoba, R.

TITLE Generation of expressed sequence tags from mouse brain

JOURNAL Unpublished

COMMENT Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkato@bs.aist-nara.ac.jp

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

source

1. .34
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0014559"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
BASE COUNT 16 a 6 c 3 g 8 t 1 others
ORIGIN

Query Match 0.9%; Score 17.6; DB 9; Length 34;
Best Local Similarity 69.7%; Pred. No. 2e+07;
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 706 TTTCAGACTAAATTTTCTTCATGCTGTGGAT 738

Db 34 TTTCAGTTTAAATGATNCTTCTTCGTAGTAGAT 2

RESULT 24

AG218655

LOCUS

34 bp DNA linear

GSS 03-SEP-2002

```

DEFINITION Drosophila melanogaster DNA, clone:NP2234-3-1, flanking P[GawB]
transposon insertion, genomic survey sequence.
ACCESSION AG218655
VERSION AG218655.1 GI:22765734
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Hayashi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H.,
Aigaki,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R.,
Uemura,T., Yoshihara,M. and Goto,S.
TITLE GETDB, a database compiling expression patterns and molecular
locations of a collection of Gal4 enhancer traps
JOURNAL Genesis (2002) In press
REFERENCE 2 (bases 1 to 34)
AUTHORS Hayashi,S.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Developmental Biology, Laboratory for Morphogenetic Signaling;
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan
(E-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,
Fax:81-78-301-3183)
COMMENT This clone was isolated from genomic DNA flanking an insertion of
the P element vector P[GawB] of a Drosophila strain.
FEATURES
Location/Qualifiers
1..34
/mol_type="genomic DNA"
/strain="NP2234"
/db_xref="taxon:7227"
/chromosome="3"
/map="93C5"
/clone="NP2234-3-1"
/note="flanking P[GawB] transposon insertion"
BASE COUNT 15 a 6 c 3 g 9 t 1 others
ORIGIN
Query Match 0.9%; Score 17.6; DB 29; Length 34;
Best Local Similarity 69.7%; Pred. No. 2e+07;
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 528 CTCGAAGCTTAAATAATCTGTAGAAAAAGCAT 560
||||| ||||| ||||| ||||| ||||| |||||
Db 1 CTCGAAGCTTAAATAATCTGTAGAAAAAGCAT 33

RESULT 25
BZ763041 35 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_111806.16.85.n Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_111806.16.85.n, genomic
survey sequence.
ACCESSION BZ763041
VERSION BZ763041.1 GI:28935594
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 35)
REFERENCE 1
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..37
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_139715.21.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"

BASE COUNT 12 a 4 c 2 g 17 t
ORIGIN
Query Match 0.9%; Score 17.6; DB 29; Length 35;
Best Local Similarity 71.9%; Pred. No. 2e+07;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1647 TTAATTTGCATTATTATGACCATAGGATT 1678
||||| ||||| ||||| ||||| ||||| |||||
Db 4 TAAATATCCATTATTATGATCATATGAAAT 35

RESULT 26
BZ768062 37 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_139715.21.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_139715.21.10.x, genomic
survey sequence.
ACCESSION BZ768062
VERSION BZ768062.1 GI:28941108
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 37)
REFERENCE 1
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..37
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_139715.21.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"

```

```

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
Atg18600.
Class: TDNA tagged.
Location/Qualifiers
1..35
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_111806.16.85.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 12 a 4 c 2 g 17 t
ORIGIN
Query Match 0.9%; Score 17.6; DB 29; Length 35;
Best Local Similarity 71.9%; Pred. No. 2e+07;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1647 TTAATTTGCATTATTATGACCATAGGATT 1678
||||| ||||| ||||| ||||| ||||| |||||
Db 4 TAAATATCCATTATTATGATCATATGAAAT 35

RESULT 26
BZ768062 37 bp DNA linear GSS 13-MAR-2003
LOCUS SALK_139715.21.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_139715.21.10.x, genomic
survey sequence.
ACCESSION BZ768062
VERSION BZ768062.1 GI:28941108
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 37)
REFERENCE 1
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..37
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_139715.21.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"

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/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 10 a 3 c 9 g 15 t

Query Match 0.9%; Score 17.6; DB 29; Length 37;
Best Local Similarity 71.9%; Pred. No. 2e+07;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 488 GTTCTTGATTCCGAAGAATCCGAGGAGATT 519

DB 1 GTTCTTGCAATTCCTAGAATGTGAGTGAGATT 32

RESULT 27
BH789828 40 bp DNA linear GSS 02-APR-2002
LOCUS SALK_046750.38.30.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_046750.38.30.x, genomic survey sequence.

ACCESSION BH789828.1 GI:19882926

VERSION BH789828

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 40)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmermann,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .40

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_046750.38.30.x"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

19 a 2 c 4 g 15 t

Query Match 0.9%; Score 17.6; DB 28; Length 40;

Best Local Similarity 65.0%; Pred. No. 2e+07;

Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1385 TTTATAGCAATTCCTTTTGAAGAAATTCAAATAGATT 1424

DB 1 TTTATAGAAATTCCTTTTATGACAAAAGTAATAGAAATT 40

RESULT 28
BZ663364/c

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK_026961.47.05.x, genomic survey sequence.

ACCESSION BZ663364

VERSION BZ663364.1

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 40)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmermann,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .40

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_026961.47.05.x"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

20 a 7 c 3 g 10 t

BASE COUNT

ORIGIN

Query Match 0.9%; Score 17.6; DB 29; Length 40;

Best Local Similarity 71.9%; Pred. No. 2e+07;

Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1466 TTAACAATACCTTCATCATCTTTTCATCGTAT 1497

DB 37 TCAGCAATGATTTCATCATGTTTGTGTTTAT 6

RESULT 29

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK_026961.47.05.x, genomic survey sequence.

ACCESSION AA863634

VERSION AA863634.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

AA863634 28 bp mRNA linear EST 11-MAR-1998
VX06C01.r1 Soares thymus 2NDMT Mus musculus cDNA clone
IMAGE:1263648 5' similar to SW:GALE_HUMAN Q14376 UDP-GLUCOSE
4-EPIMERASE ; mRNA sequence.

AA863634

VERSION AA863634.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:666200

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 23.

FEATURES

source

1. .28
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1263648"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares thymus 2Nbmt"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[Pharmacia], digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
5 a 10 c 6 g 7 t

BASE COUNT
ORIGIN

Query Match 0.9%; Score 17.4; DB 9; Length 28;
Best Local Similarity 77.8%; Pred. No. 2.1e+07;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1803 CTTTGGACTTTAGTCCCAAGGCC 1829

||||| ||||| ||||| ||||| ||||| |||||

Db 2 CTTTCGTACTTCAATCCCATAGCGCC 28

RESULT 30

BH866003

LOCUS

DEFINITION SALK_100228 Arabidopsis thaliana DNA linear GSS 05-AUG-2002
thaliana genomic clone SALK_100228, genomic survey sequence.

ACCESSION BH866003

VERSION BH866003.1

KEYWORDS GI:22101901

SOURCE GSS.

ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1 (bases 1 to 35)

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab
C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.
Zimmerman, J. and Ecker, J.R.

A Sequence-indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .35

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_100228"

/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

10 a 6 c 11 g 8 t

Query Match 0.9%; Score 17.4; DB 28; Length 35;

Best Local Similarity 77.8%; Pred. No. 2.2e+07;

Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 241 AGAGACGATCTCTCTGATCTTTGGAA 267

||||| ||||| ||||| ||||| |||||

Db 7 ACAGACGAGCTCTGTAAGTTGGAA 33

BH864481 38 bp DNA linear GSS 05-AUG-2002

SALK_096115 Arabidopsis thaliana TDNA insertion lines Arabidopsis

thaliana genomic clone SALK_096115, genomic survey sequence.

BH864481

VERSION BH864481.1

KEYWORDS GI:22100379

SOURCE GSS.

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 38)

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab

C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.

Zimmerman, J. and Ecker, J.R.

A Sequence-indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .38

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_096115"

FEATURES

source

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 11 a 6 c 11 g 10 t

ORIGIN

Query Match 0.9%; Score 17.4; DB 28; Length 38;
Best Local Similarity 77.8%; Pred. No. 2.2e+07;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 241 AGAGACGATCTTCTGATCTTGGAA 267

||||||| ||| ||| ||| ||| ||| |||

Db 10 AGAGACGAGCTCGTAAAGTTGGAA 36

RESULT 32

AZ772005/c

LOCUS

DEFINITION 1M0574P02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0574P02 R, genomic survey sequence.

ACCESSION AZ772005.1 GI:12894867

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 39)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0574 row: P column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 39.

Location/Qualifiers

1. .39

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0574P02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 6 a 5 c 7 g 21 t

ORIGIN

Query Match 0.9%; Score 17.4; DB 28; Length 39;
Best Local Similarity 77.8%; Pred. No. 2.2e+07;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 533 AGCTTTAAAAAATCTGTAGAAAAAGGA 559

||||| ||| ||| ||| ||| ||| |||

Db 39 AGCCCCAAAAAATCTAAACAAAAAGGA 13

RESULT 33

AZ345478

LOCUS

DEFINITION 1M0080A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080A01 F, genomic survey sequence.

ACCESSION AZ345478

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: A column: 01

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 40.

Location/Qualifiers

1. .40

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080A01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

LOCUS	AU265359	31 bp	mRNA	linear	EST 10-MAY-2002
DEFINITION	AU265359	VS	Dictyostelium discoideum	cDNA clone VSP523	5', mRNA sequence.
ACCESSION	AU265359				

Query Match 0.9%; Score 17.2; DB 28; Length 30;
Best Local Similarity 73.3%; Pred.No. 2.4e+07;
Matches 22; Conservative 0; Mismatches 8; Indels

AU265359/C	AU265359	31 bp	mRNA	linear	EST 10-MAY-2002
LOCUS	AU265359				
DEFINITION	AU265359	VS	Dictyostelium discoideum	cDNA clone VSF523	5', mRNA
ACCESSION	AU265359				

```

VERSION AU265359.1 GI:20524157
KEYWORDS EST
SOURCE Dictyostellium discoideum
ORGANISM Dictyostellium discoideum
REFERENCE 1 (bases 1 to 31)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
        Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
        Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
        stages of Dictyostellium discoideum
JOURNAL Unpublished
COMMENT Contact: Hideko Urushihara
        Institute of Biological Sciences
        University of Tsukuba
        1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
        Tel: 81-298-53-4664
        Fax: 81-298-53-6614
        Email: hideko@biol.tsukuba.ac.jp.
FEATURES
        source
            1..31
            /organism="Dictyostellium discoideum"
            /mol_type="mRNA"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="VSF523"
            /sex="mat A"
            /dev_stage="vegetative"
            /clone_lib="VS"
BASE COUNT 15 a 6 c 1 g 8 t 1 others
ORIGIN
Query Match 0.9%; Score 17.2; DB 9; Length 31;
Best Local Similarity 86.4%; Pred. No. 2.4e+07;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 GTGTTTCTTTAGGTTCGGT 861
    |||||
Db 29 GTTTTTTTTAAAGTTCGT 8

RESULT 37
C00007 HUMGS0002225 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
LOCUS sequence.
DEFINITION C00007
ACCESSION C00007.1 GI:1432237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Okubo,K.
JOURNAL BodyMap; human gene expression database
COMMENT Unpublished
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see: http://www.imcb.osaka-u.ac.jp/bodymap/. The
sequences of the clones represented by this GS sequences is also
found there.
FEATURES
        source
            1..33
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"

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/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
BASE COUNT 8 a 8 c 3 g 14 t
ORIGIN
Query Match 0.9%; Score 17.2; DB 14; Length 33;
Best Local Similarity 73.3%; Pred. No. 2.4e+07;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1414 TCAATAGATTGCAAGCCATTGGTTCCTT 1443
    |||||
Db 3 TCAATAAATTGTATGCTTTCCTCCTCT 32

RESULT 38
AZ481068 36 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0303L03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0303L03 F, genomic survey sequence.
ACCESSION AZ481068
VERSION AZ481068.1 GI:10642133
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
        1 (bases 1 to 36)
        Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
        ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
        and Wright,D., Weiss,R.
        Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
        Unpublished
        Contact: Robert B. Weiss
        University of Utah Genome Center
        University of Utah
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5606
        Fax: 801 585 7177
        Email: rdunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0303 row: L column: 03
        Seq primer: CGTTGTAACGACGCGCCAGT
        Class: plasmid ends
        High quality sequence stop: 36.
FEATURES
        source
            1..36
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0303L03"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid F1. The vector was ligated
            with adaptors complementary to the insert adaptors and

```

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 6 c 10 g 8 t

ORIGIN

Query Match 0.9%; Score 17.2; DB 28; Length 36;
Best Local Similarity 86.4%; Pred. No. 2.4e+07;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 751 ACATACAGATTGTCATATGATG 772

Db 15 ACACACACATTTGTCATGTGATG 36

RESULT 39

AZ317175/c

LOCUS AZ317175 38 bp DNA linear GSS 29-SRP-2000
DEFINITION 1M0035H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0035H16 R, genomic survey sequence.

ACCESSION AZ317175.1 GI:10365723

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0035 row: H column: 16

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 38.

Location/Qualifiers

FEATURES

source

1..38

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0035H16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 6 a 16 c 7 g 9 t

ORIGIN

Query Match 0.9%; Score 17.2; DB 28; Length 38;
Best Local Similarity 73.3%; Pred. No. 2.5e+07;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 813 GCACAAAACCTTGGGCTGTTCTGGAAGTG 842

Db 38 GCAGAGAACTCTGGCAGCTGCTGGAGATG 9

RESULT 40

AZ583903/c

LOCUS

DEFINITION 1M0388P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0388P03 F, genomic survey sequence.

ACCESSION AZ583903

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0388 row: P column: 03

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 38.

Location/Qualifiers

FEATURES

source

1..38

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0388P03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number


```
/lab_host="DH10B"  
/clone_lib="NCI_CGAP_Mam2"  
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;  
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"
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BASE COUNT      11 a      7 c      10 g      12 t
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ORIGIN

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Query Match      0.9%; Score 17.2; DB 12; Length 40;  
Best Local Similarity 73.3%; Pred. No. 2.5e+07;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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QY      475 CGTAGATGCAAAATGTTCTTGTATTTCGAAAG 504
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Db      30 CGGTGAAGCTGATATTCTTGTATTCAACAG 1
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Search completed: October 23, 2003, 12:34:16  
Job time : 3606 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: October 23, 2003, 08:19:59 ; Search time 6720 Seconds
(without alignments)
11347.551 Million cell updates/sec

Title: US-09-868-987-1
Perfect score: 1864
Sequence: 1 atggacttcgcgattgtgc.....atgcacaaattcagataatgc 1864

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 1197658

Minimum DB seq length: 10
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rod.*
- 36: em.htg_man.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20.6	1.1	38	6	AX082473 Sequence
C 2	20.4	1.1	33	6	AX004499 Sequence
C 3	20.4	1.1	33	6	AX004508 Sequence
C 4	20.4	1.1	34	6	AX236522 Sequence
C 5	20.4	1.1	40	6	BD179478 Gene expr
C 6	20.4	1.1	40	6	178765 Sequence 21
C 7	20.4	1.1	40	6	192057 Sequence 24
C 8	20	1.1	20	6	AR312098 Sequence
C 9	20	1.1	20	6	AR314596 Sequence
C 10	20	1.1	20	6	AR314597 Sequence
C 11	20	1.1	20	6	AR315797 Sequence
C 12	19.8	1.1	40	6	AX394952 Sequence
C 13	19.2	1.0	35	6	BD176659 Promoter.
C 14	19	1.0	27	6	AR183406 Sequence
C 15	19	1.0	35	6	AX468186 Sequence
C 16	19	1.0	40	8	ATH552627 Arabidops
C 17	18.8	1.0	31	6	AR095717 Sequence
C 18	18.8	1.0	31	6	AR145333 Sequence
C 19	18.8	1.0	39	6	AX453607 Sequence
C 20	18.8	1.0	40	6	E27307 DNA polymer
C 21	18.6	1.0	37	6	AX581933 Sequence
C 22	18.6	1.0	37	9	AF505528 Homo sapi
C 23	18.6	1.0	38	6	A22367 oligonucleo
C 24	18.6	1.0	38	6	AR069295 Sequence
C 25	18.6	1.0	38	6	AR076115 Sequence
C 26	18.6	1.0	38	6	I18853 Sequence 34
C 27	18.6	1.0	38	6	I22307 Sequence 34
C 28	18.4	1.0	34	6	AX528937 Sequence
C 29	18.4	1.0	38	6	AR027048 Sequence
C 30	18.4	1.0	40	6	AX515048 Sequence
C 31	18.4	1.0	40	6	AX520873 Sequence
C 32	18.4	1.0	40	6	E27309 DNA polymer
C 33	18.2	1.0	33	6	AX419814 Sequence
C 34	18.2	1.0	34	8	ATH524156 Arabidops
C 35	18.2	1.0	36	6	BD007105 Targeted
C 36	18.2	1.0	36	6	BD007113 Targeted
C 37	18	1.0	32	6	AX322217 Sequence
C 38	18	1.0	34	6	AX236755 Sequence
C 39	18	1.0	38	6	AX580535 Sequence
C 40	17.8	1.0	31	6	AX249610 Sequence
C 41	17.8	1.0	37	6	AR279589 Sequence
C 42	17.8	1.0	37	6	AX002911 Sequence
C 43	17.8	1.0	37	6	AX018237 Sequence
C 44	17.8	1.0	37	6	AX183756 Sequence
C 45	17.8	1.0	38	6	AX228781 Sequence

ALIGNMENTS

RESULT 1
AX082473/c
LOCUS AX082473 38 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 11 from Patent WO0111060.
ACCESSION AX082473
VERSION AX082473.1 GI:13184620
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ravn,P., Madsen,S.M., Vrang,A., Israelsen,H., Johnsen,M.G.,
Bredmose,L. and Arnau,J.
TITLE Method of isolating secretion signals in lactic acid bacteria, and
secretion signals isolated from lactococcus lactis

BASE COUNT	10 a	8 c	9 g	6 t
ORIGIN				
Query Match	1.1%;	Score 20.4;	DB 6;	Length 33;
Best Local Similarity	80.0%;	Pred. No. 7.3e+06;		
Matches	24; Conservative	0; Mismatches	6; Indels	0; Gaps
Qy	862	TGCTCTCGGGTTTGGAGCCTGGAATTCGTT	891	
Db	33	TGCTCTCTGGGTTGCCACCTGGAATTCAGT	4	
RESULT 4				
AX236522/c				
LOCUS	AX236522	34 bp	DNA	linear
DEFINITION	Sequence 215 from Patent WO0164922.			PAT 26-SEP-2001
ACCESSION	AX236522			
VERSION	AX236522.1	GI:15796108		
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1			
AUTHORS	Arico, M.B., Comanducci, M.C., Galeotti, C.C., Masignani, V.C.,			
TITLE	Guilian, M.M. and Pizzi, M.C.			
JOURNAL	Heterologous expression of neisserial proteins			
FEATURES	Patent: WO 0164922-A 215 07-SEP-2001;			
	Chiron Spa (IT)			
	Location/Qualifiers			
	1..34			
	/organism="synthetic construct"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:32630"			
	/note="Oligonucleotide"			
BASE COUNT	14 a	5 c	6 g	9 t
ORIGIN				
Query Match	1.1%;	Score 20.4;	DB 6;	Length 34;
Best Local Similarity	80.0%;	Pred. No. 7.3e+06;		
Matches	24; Conservative	0; Mismatches	6; Indels	0; Gaps
Qy	1646	TTTAATTTTGCATTATTATGACCATAGG	1675	
Db	34	TTCAATTTTGTATATTTTATGACCATATGG	5	
RESULT 5				
BD179478/c				
LOCUS	BD179478	40 bp	DNA	linear
DEFINITION	Gene expression control unit and use thereof.			PAT 16-APR-2003
ACCESSION	BD179478			
VERSION	BD179478.1	GI:30016796		
KEYWORDS	WO 02086131-A/30.			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 40)			
AUTHORS	Yamamoto, M., Watanabe, D., Teranishi, Y. and Nakanishi, S.			
TITLE	Gene expression control unit and use thereof			
JOURNAL	Patent: WO 02086131-A 30 31-OCT-2002;			
	GENCOM CORP, MUTSUVA YAMAMOTO, DAI WATANABE, YUTAKA TERANISHI,			
	SHIGETA NAKANISHI			
COMMENT	OS Artificial Sequence			
	FN WO 02086131-A/30			
	PD 31-OCT-2002			
	PF 09-APR-2002			
	PR 09-APR-2001			
	PI MUTSUVA YAMAMOTO, DAI WATANABE, YUTAKA TERANISHI, SHIGETA			
	NAKANISHI			
	PC C12N15/85, C12N5/10, G01N33/50, G01N33/68, A01K67/027 CC			
	Description of Artificial Sequence: Synthesized FH Key			
	Location/Qualifiers			
	FT source			
	1..40			

DB	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	/organism='Artificial Sequence'
BASE COUNT	7	a 11 c 8 g 14 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	545	TCCTGAGAAAAAGCATATACCAAGCCTTTTGAGCCAT	582
Db	40	TCATTAGATAAAGGATACAATAAGCGCGCCGAGCCAT	3
RESULT 6			
I78765/c			
LOCUS	I78765	Sequence 21 from patent US 5693781.	linear PAT 03-APR-1998
DEFINITION	I78765		
ACCESSION	I78765		
VERSION	I78765.1	GI:3014919	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 40)		
AUTHORS	Zupancic,T.J. and Yukawa,H.		
TITLE	Promoter DNA fragment from coryneform bacteria		
JOURNAL	Patent: US 5693781-A 21 02-DEC-1997;		
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
RESULT 7			
I92057/c			
LOCUS	I92057	Sequence 24 from patent US 5726299.	linear PAT 01-DEC-1998
DEFINITION	I92057		
ACCESSION	I92057		
VERSION	I92057.1	GI:3936527	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 40)		
AUTHORS	Zupancic,T.J. and Yukawa,H.		
TITLE	Promoter DNA fragment from coryneform bacteria		
JOURNAL	Patent: US 5726299-A 24 10-MAR-1998;		
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			
Query Match	1.1%; Score 20.4; DB 6;	Length 40;	
Best Local Similarity	71.1%; Pred. No. 7.2e+06;		
Matches	27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
QY	1038	TTGGATCTTCAGAAAAGATCAAAATCTATTATTAGTGAT	1075
Db	39	TGGGATCCGTAGAAAAGATCAAAAGTCTTTCTTGAGAT	2
FEATURES	source	Location/Qualifiers	
BASE COUNT	10	a 10 c 7 g 13 t	
ORIGIN			

REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5134 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 5 a 6 c 5 g 4 t
ORIGIN

Query Match 1.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1568 TTCAGCGCGACGTAATGAC 1587
Db 1 TTCAGCGCGACGTAATGAC 20
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RESULT 11
AR315797/c
LOCUS AR315797 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6334 from patent US 6559294.
ACCESSION AR315797
VERSION AR315797.1 GI:31709223
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6334 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 5 a 6 c 4 g 5 t
ORIGIN

Query Match 1.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ATTCTGCAACCGTGATGG 73
Db 20 ATTCTGCAACCGTGATGG 1
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RESULT 12
AX394952
LOCUS AX394952 40 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 89 from Patent WO0218595.
ACCESSION AX394952
VERSION AX394952.1 GI:21066025
KEYWORDS
SOURCE Synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Loomore,S., Wang,J., Bradley,B., Ochs,M. and Yang,Y.P.
TITLE Moraxella polypeptides and corresponding dna fragments and uses thereof
JOURNAL Patent: WO 0218595-A 89 07-MAR-2002;
Aventis Pasteur Limited (CA)
FEATURES Location/Qualifiers
source 1..40
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="5' PCR primer for MCA101924"
BASE COUNT 6 a 2 c 14 g 18 t

ORIGIN

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Best Local Similarity 77.4%; Pred. No. 9.7e+06;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 310 GGCAATGCTTATTGTTTTCATGAGCGTATAT 340
Db 1 GGCAATTCATATGTTTTCATGAGCGTATAT 31
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RESULT 13
BD176659
LOCUS BD176659 35 bp DNA linear PAT 18-MAR-2003
DEFINITION Promoter.
ACCESSION BD176659
VERSION BD176659.1 GI:29122369
KEYWORDS WO 02072819-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 35)
AUTHORS Shimojo,T., Takakura,H., Ochiai,K., Asada,K. and Ka,I.
TITLE Promoter
JOURNAL Patent: WO 02072819-A 28 19-SEP-2002;
TAKARA SHUZO CO LTD.TOMOKO SHIMOJO,HIKARU TAKAKURA,KAZUYORI OCHIAI,
KIYOZO ASADA,IKUNOSHIN KATO
COMMENT OS Artificial Sequence
PN WO 02072819-A/28
PF 13-MAR-2002 WO 2002JP002341
PR 14-MAR-2001 JP 01P 072802
PI TOMOKO SHIMOJO,HIKARU TAKAKURA,KAZUYORI OCHIAI,KIYOZO ASADA,
PI IKUNOSHIN KATO
PC C12N15/09,C12N1/19,C12N1/21,C12N5/10,C12P21/02 CC
Description of Artificial Sequence: A sequence of primer AP7R1
CC for
CC amplifying coding region of nitrophenyl phosphatase gene. FH
Key Location/Qualifiers
FT source 1..35
/organism='Artificial Sequence'.
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 6 a 14 c 10 g 5 t
ORIGIN

Query Match 1.0%; Score 19.2; DB 6; Length 35;
Best Local Similarity 75.0%; Pred. No. 1.3e+07;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 418 GGATCGCCACTTCACCTTGTTCAGGACTCGCTG 449
Db 3 GGACGCGTCACCCCTCTCTGCAGAACTCGCTG 34
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RESULT 14
AR183406/c
LOCUS AR183406 27 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6340747.
ACCESSION AR183406
VERSION AR183406.1 GI:20226999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 27)
AUTHORS Bazin,H. and Mathis,G.
TITLE Fluorescent conjugates of nucleosides or nucleotides, process for their preparation and their uses
JOURNAL Patent: US 6340747-A 2 22-JAN-2002;

JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gascon Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplatne' (<http://www.genoplatne.com> and <http://genoplatne-info.inbioigen.fr>).

FEATURES

source Location/Qualifiers

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/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Wassiljewskija"

/db_xref="taxon:3702"

/clone="J40D04"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature 1..40

/note="T-DNA flanking sequence

left border"

11 a 7 c 2 g 20 t

BASE COUNT

ORIGIN

Query Match 1.0%; Score 19; DB 8; Length 40;

Best Local Similarity 71.4%; Pred. No. 1.5e+07;

Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1050 AAAAGATCAAAATCTATTTTAGTGATAAAGCTTTA 1084

Db 1 AACTTATCAATATCCATCTTATTGATCATTCCTTTA 35

RESULT 17

AR095717

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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/organism="unknown"

6 a 7 c 8 g 10 t

BASE COUNT

ORIGIN

Query Match 1.0%; Score 18.8; DB 6; Length 31;

Best Local Similarity 76.7%; Pred. No. 1.7e+07;

Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 852 TAGGTTTCGCTTGCTCGGGTTTGGAGCCT 881

Db 2 TAGGTTTCAGTCGACTCGAGATTGGATCCT 31

RESULT 18

AR145333

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

AR145333

Sequence 12 from patent US 6211351.

AR145333.1 GI:15107200

Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Kumar, R. and Metz, R. A.
TITLE Chimeric mutational vectors
JOURNAL Patent: US 6211351-A 12 03-APR-2001;
FEATURES
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BASE COUNT 6 a 7 c 8 g 10 t
ORIGIN
    Query Match 1.0%; Score 18.8; DB 6; Length 31;
    Best Local Similarity 76.7%; Pred. No. 1.7e+07;
    Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 852 TAGGTTCCGTTGCTCTCGGTTTGGACCT 881
    ||||| | ||| ||||| ||||| |||||
Db 2 TAGGTTTCAGTGCACTCGAGATTGGATCCT 31

RESULT 19
AX53607 AX453607 39 bp DNA linear PAT 06-JUL-2002
LOCUS
DEFINITION Sequence 7 from Patent WO0231158.
ACCESSION AX453607
VERSION AX453607.1 GI:21712845
KEYWORDS Corynebacterium glutamicum
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1
AUTHORS Hanke, P. D.
TITLE Feedback-resistant pyruvate carboxylase gene from Corynebacterium
JOURNAL Patent: WO 0231158-A 7 18-APR-2002;
ARCHER-DANIELS-MIDLAND COMPANY (US)
FEATURES
    source
        1..39
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        /mol_type="genomic DNA"
        /db_xref="taxon:1718"
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ORIGIN
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    Best Local Similarity 76.7%; Pred. No. 1.6e+07;
    Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1337 GCGGTATGCGCTTTAATTCATGACCTTTG 1366
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Db 2 GCGGTATGCGCTTTGTTTCTTTCACCTGATG 31

RESULT 20
E27307/c
LOCUS
DEFINITION DNA polymerase gene.
ACCESSION E27307
VERSION E27307.1 GI:13026438
KEYWORDS JP 1999151087-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Yoshizumi, I.
TITLE DNA polymerase gene
JOURNAL Patent: JP 1999151087-A 1 08-JUN-1999;
TAKARA SHUZO CO LTD
COMMENT OS Unidentified
PN JP 1999151087-A/1
PD 08-JUN-1999
PF 19-NOV-1997 JP 1997318665

PR YOSHIZUMI ISHINO
PI C12N15/09, C12N1/21, C12N9/12// (C12N15/09, C12R1.01), (C12N1/21,
PC C12R1.19),
PC (C12N9/12, C12R1.19), C12N15/00, (C12N15/00, C12R1.01) CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..40
FT /organism="Unidentified".
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        1..40
        /organism="Unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
BASE COUNT 19 a 2 c 9 g 10 t
ORIGIN
    Query Match 1.0%; Score 18.8; DB 6; Length 40;
    Best Local Similarity 68.4%; Pred. No. 1.6e+07;
    Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1646 TTTAATTTGCATTTTATTATGACCATGAGGATTTCTTCT 683
    ||||| | ||||| ||||| ||||| |||||
Db 40 TCTAAGAATTTTATTATTATCTCCATATGTATCCTCCT 3

RESULT 21
AX581933
LOCUS
DEFINITION Sequence 3771 from Patent WO0211674.
ACCESSION AX581933
VERSION AX581933.1 GI:27653743
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D. E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (Cica-1)
JOURNAL Patent: WO 0211674-A 3771 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
FEATURES
    source
        1..37
        /organism="synthetic construct"
        /mol_type="mrna"
        /db_xref="taxon:32630"
        /note="Enzymatic Nucleic Acid"
BASE COUNT 10 a 6 c 10 g 11 t
ORIGIN
    Query Match 1.0%; Score 18.6; DB 6; Length 37;
    Best Local Similarity 72.7%; Pred. No. 1.8e+07;
    Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1812 TTTAGTCCCAAGGCCCTGTGGTATTAAATTT 1844
    ||||| ||||| ||||| ||||| |||||
Db 4 TTCAGGCCGAAGCGAGTGAGTGCTTAACTTT 36

RESULT 22
AF505528
LOCUS
DEFINITION Homo sapiens clone Y1.7 T cell receptor gamma CDR3 region sequence.
ACCESSION AF505528
VERSION AF505528.1 GI:30269382
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS Dare,R.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2002) Hematology & Genetic Pathology, Flinders University of South Australia, Flinders Medical Centre, Flinders Drive, Bedford Park, South Australia 5042, Australia
FEATURES
source Location/Qualifiers
1..37
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Y1.7"
misc_feature 1..37
/cell_type="peripheral blood T cell"
misc_feature 1..12
/note="T cell receptor gamma CDR3 region"
misc_feature 13..18
/note="Region: V4"
misc_feature 19..37
/note="Region: N"
misc_feature 19..37
/note="Region: J1/2"
BASE COUNT 13 a 6 c 7 g 11 t
ORIGIN
Query Match 1.0%; Score 18.6; DB 9; Length 37;
Best Local Similarity 72.7%; Pred. No. 1.8e+07;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1133 AGCTGCGTTATGTGGGATTGTTGCAGAAAC 1165
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Db 3 ACCTGGGATGTTAGTAATTATTATAGAAAC 35
RESULT 23
LOCUS A22367 38 bp DNA linear PAT 04-MAY-1995
DEFINITION oligonucleotide K54 from patent WO9220805.
ACCESSION A22367
VERSION A22367.1 GI:904247
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 38)
AUTHORS St.ang hl S.; Nygren, P.-A.; Hansson, M.; Uhlen, M. and Nguyen, T. Ngoc.
TITLE Recombinant DNA coding for signal peptide, selective interacting polypeptide and membrane anchoring sequence
JOURNAL Patent: US 5958736-A 4 28-SEP-1999;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
BASE COUNT 6 a 9 c 9 g 14 t
ORIGIN
Query Match 1.0%; Score 18.6; DB 6; Length 38;
Best Local Similarity 72.7%; Pred. No. 1.8e+07;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 848 CTTTATAGTTGCGTCTCTCGGGTTTGAGCC 880
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Db 6 CTTTATAGTCTCTTTCAGTTTCCAGCTTGTGTC 38
RESULT 24
LOCUS AR069295/c 38 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5891631.
ACCESSION AR069295
VERSION AR069295.1 GI:7220183
KEYWORDS

Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Goldstein,J.L.; Brown,M.S.; Briggs,M.R. and Wang,X.
TITLE Methods relating tosterol regulatory element binding proteins
JOURNAL Patent: US 5891631-A 34 06-APR-1999;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
BASE COUNT 7 a 4 c 14 g 13 t
ORIGIN
Query Match 1.0%; Score 18.6; DB 6; Length 38;
Best Local Similarity 72.7%; Pred. No. 1.8e+07;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 121 AAACGTCCCATTTGAAAAATCATGCCAGTGTCTC 153
|||||
Db 35 AATCACCCCACTGTAAATATCACCCCACTGTGTC 3
RESULT 25
LOCUS AR076115 38 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 4 from patent US 5958736.
ACCESSION AR076115
VERSION AR076115.1 GI:10002861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS St.ang hl S.; Nygren, P.-A.; Hansson, M.; Uhlen, M. and Nguyen, T. Ngoc.
TITLE Recombinant DNA coding for signal peptide, selective interacting polypeptide and membrane anchoring sequence
JOURNAL Patent: US 5958736-A 4 28-SEP-1999;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
BASE COUNT 6 a 9 c 9 g 14 t
ORIGIN
Query Match 1.0%; Score 18.6; DB 6; Length 38;
Best Local Similarity 72.7%; Pred. No. 1.8e+07;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 848 CTTTATAGTTGCGTCTCTCGGGTTTGAGCC 880
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Db 6 CTTTATAGTCTCTTTCAGTTTCCAGCTTGTGTC 38
RESULT 26
LOCUS I18853/c 38 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 34 from patent US 5498696.
ACCESSION I18853
VERSION I18853.1 GI:1599208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Briggs,M.R.; Brown,M.S.; Goldstein,J.L. and Wang,X.
TITLE Sterol regulatory element binding proteins and their use in screening assays
JOURNAL Patent: US 5498696-A 34 12-MAR-1996;
FEATURES Location/Qualifiers
source 1..38
/organism="unknown"
BASE COUNT 7 a 4 c 14 g 13 t
ORIGIN


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misc_feature 1..34
/notes="T-DNA flanking sequence
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BASE COUNT 12 a 5 c 5 g 12 t
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Query Match 1.0%; Score 18.2; DB 8; Length 34;
Best Local Similarity 74.2%; Pred. No. 2.2e+07;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 534 GTCTTAAAAAATCTGTAGAAAAGGATATAC 564
|||||
Db 34 GTCTTAATATCTCTAGGACAATAATGTAC 4

RESULT 35
BD007105/c
LOCUS Targeted cytotoxic cells. 36 bp DNA linear PAT 31-JAN-2002
DEFINITION BD007105
ACCESSION BD007105.1 GI:18635476
VERSION BD007105.1
KEYWORDS JP 2001503978-A/20.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Chen,S.
TITLE Targeted cytotoxic cells
JOURNAL Patent: JP 2001503978-A 20 27-MAR-2001;
COMMENT WAKE FOLEST UNIVERSITY
OS Unidentified
PN JP 2001503978-A/20
PD 27-MAR-2001
PF 23-OCT-1997 JP 1998519647
PR 23-OCT-1996 US 08/740003
PI SHII CHEN
PC C12N15/09,A61K35/30,A61K38/00,A61P31/12,A61P31/18,
PC A61P35/00,
PC A61P43/00,C12N5/10,C12N15/00,C12N5/00,A61K37/02 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..36
FT /organism='Unidentified'.

Query Match 1.0%; Score 18.2; DB 6; Length 36;
Best Local Similarity 74.2%; Pred. No. 2.2e+07;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 998 GAAGCTGGTCTTTCTCTAGAGACTTCGGTA 1028
|||||
Db 33 GAAGCTGACGTCGCCTCTAGAGAATTCGGTA 3

RESULT 37
AX322217/c
LOCUS AX322217
DEFINITION Sequence 90 from Patent EP1162276.
ACCESSION AX322217
VERSION AX322217.1 GI:18093283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kramer,M.D., Winter,H. and Reinhartz,J.
TITLE Mrna molecules to be used as indicators of the functional and
activation state of t-lymphocytes
JOURNAL Patent: EP 1162276-A 90 12-DEC-2001;
Lynx Therapeutics GmbH (DE)
FEATURES
source 1..32
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
BASE COUNT 14 a 6 c 6 g 6 t
ORIGIN
Query Match 1.0%; Score 18; DB 6; Length 32;
Best Local Similarity 80.8%; Pred. No. 2.5e+07;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1592 GCTACAACCTATCATCGTTTGTGTAAT 1617
|||||
Db 27 GCTAGCAGTCTATCAATTTGTGAT 2

RESULT 38
AX236755/c
LOCUS AX236755
DEFINITION Sequence 448 from Patent WO0164922.
ACCESSION AX236755
TITLE Targeted cytotoxic cells. 36 bp DNA linear PAT 31-JAN-2002
DEFINITION BD007113
ACCESSION BD007113
VERSION BD007113.1 GI:18635484
KEYWORDS JP 2001503978-A/28.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Chen,S.
```


ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 016800-A 1689 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source 1..31
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 11 a 7 c 3 g 9 t 1 others
ORIGIN

Query Match 1.0%; Score 17.8; DB 6; Length 31;
Best Local Similarity 75.9%; Pred. No. 2.7e+07;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1400 TTTTTCGAAGAAATTCAAATAGATTTGCA 1428
|||||
Db 29 TTTTTCGAACAATCAGGTTATGTGCA 1
|||||

RESULT 41
AR279589 37 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 11 from patent US 6517829.
ACCESSION AR279589
VERSION AR279589.1 GI:29714479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 37)
AUTHORS Frenken, L.G.J., Harmsen, M.M., van der Linden, R.H.J. and Verrips, C.T.
TITLE Products comprising inactivated yeasts or moulds provided with active antibodies
JOURNAL Patent: US 6517829-A 11 11-FEB-2003;
FEATURES Location/Qualifiers
source 1..37
/organism="unknown"
BASE COUNT 4 a 6 c 14 g 13 t
ORIGIN

Query Match 1.0%; Score 17.8; DB 6; Length 37;
Best Local Similarity 75.9%; Pred. No. 2.7e+07;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 877 AGCCTCGAATTCGTTTGGGATGGATT 905
|||||
Db 8 AGCCTTGGATTCGTTGTAGGATGGGTT 36
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RESULT 42
AX002911 37 bp DNA linear PAT 24-AUG-2000
LOCUS
DEFINITION Sequence 11 from Patent EP0954978.
ACCESSION AX002911
VERSION AX002911.1 GI:9926827
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Harmsen, M.M. and Frenken, L.G.
TITLE New products comprising inactivated yeasts or moulds provided with active antibodies
JOURNAL Patent: EP 0954978-A 11 10-NOV-1999;
UNILEVER PLC (GB); UNILEVER NV (NL)
FEATURES Location/Qualifiers

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source
1. .37
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="primer_bind"
4 a 6 c 14 g 13 t
BASE COUNT
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Query Match
Best Local Similarity 1.0%; Score 17.8; DB 6; Length 37;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 877 AGCCTGGAATTCGTTTGGGAATGGATT 905
|||||
Db 8 AGCCTTGGATTCGTTCTAGGATTGGGTT 36
|||||

RESULT 43
AX018237
LOCUS 37 bp DNA linear PAT 07-SEP-2000
DEFINITION
Sequence 11 from Patent WO9946300.
ACCESSION
AX018237
VERSION
AX018237.1 GI:10042576
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Harmeen,M.M., Convents,D., Frenken,L.G., Van Der Linden,R.H. and
Verrips,T.C.
TITLE
Products comprising inactivated yeasts or moulds and active
vhh-type antibodies
JOURNAL
UNILEVER PLC (GB); HARMSSEN MICHAEL MARIE (NL); UNILEVER NV (NL);
CONVENTS DANIEL (NL); FRENKEN LEON GERARDUS JOSEPH (NL); LINDEN
RICHARD HENRICUS JACOBUS (NL); VERRIPS THEODORUS CORNELIS (NL)
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="primer_bind"
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BASE COUNT
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Query Match
Best Local Similarity 1.0%; Score 17.8; DB 6; Length 37;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 877 AGCCTGGAATTCGTTTGGGAATGGATT 905
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Db 8 AGCCTTGGATTCGTTCTAGGATTGGGTT 36
|||||

RESULT 44
AX183756/c
LOCUS 37 bp DNA linear PAT 06-AUG-2001
DEFINITION
Sequence 1509 from Patent WO0142511.
ACCESSION
AX183756
VERSION
AX183756.1 GI:15135081
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE
Ibd-related polymorphisms
JOURNAL
Patent: WO 0142511-A 1509 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
Location/Qualifiers
source
1. .37
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="primer_bind"
4 a 6 c 14 g 13 t
BASE COUNT
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Best Local Similarity 1.0%; Score 17.8; DB 6; Length 37;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 877 AGCCTGGAATTCGTTTGGGAATGGATT 905
|||||
Db 8 AGCCTTGGATTCGTTCTAGGATTGGGTT 36
|||||

RESULT 45
AX228781/c
LOCUS 38 bp mRNA linear PAT 10-SEP-2001
DEFINITION
Sequence 2153 from Patent WO0157206.
ACCESSION
AX228781
VERSION
AX228781.1 GI:15557922
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boober,R.N. and Holman,P.S.
TITLE
Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL
Patent: WO 0157206-A 2153 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
source
1. .38
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
16 a 8 c 10 g 4 t
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 1.0%; Score 17.8; DB 6; Length 38;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 583 TTTTGATTCTAACTTGACTACAGTATTGGCCTCAGCA 619
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Db 38 TTTTGTGTAGACCTTGACTCGCCTTCGGCTTCGGCA 2
|||||

Search completed: October 23, 2003, 11:34:00
Job time : 6723 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 06:27:44 ; Search time 499 Seconds
(without alignments)
10083.672 Million cell updates/sec

Title: US-09-868-987-1

Perfect score: 1864

Sequence: 1 atggacttcgcatattgtc.....atgacaaattcagataatgc 1864

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2322168

Minimum DB seq length: 10

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20.6	1.1	38	22	AAF59470
C 2	20.4	1.1	33	20	AAF91515
C 3	20.4	1.1	34	22	AA343955
C 4	20.4	1.1	40	16	AA080353
C 5	20.4	1.1	40	18	AA792927
C 6	20.4	1.1	40	25	AB225344
C 7	20	1.1	20	20	AA97008
C 8	20	1.1	20	20	AA95807

L. lactis novel se
Bovine interferon-
Neisseria meningit
Synthetic promoter
Synthetic promoter
PCR primer MYK107,
PCR primer used to
PCR primer used to

ALIGNMENTS

RESULT 1

AAF59470/C

ID AAF59470 standard; DNA; 38 Bp.

XX

AC AAF59470;

XX

DT 03-MAY-2001 (first entry)

XX

DE L. lactis novel secretion signal isolation related PCR primer SEQ.11.

XX

XX Lactococcus lactis; signal peptide; secretion signal; SP310; mutant;

KW lactic acid bacterium; promoterless promoter reporter; PPR; transposon;

KW identification; secretion reporter; site directed mutagenesis;

KW PCR primer; ss.

XX

XX Lactococcus lactis.

OS Synthetic.

XX

PN WO200111060-A2.

XX

PD 15-FEB-2001.

XX

PF 04-AUG-2000; 2000WO-DK00437.

XX

PR 06-AUG-1999; 99DK-0001105.

XX

PA (BIOT-) BIOTEKNOLOGISK INST.

XX

XX Ravn P, Madsen SM, Vrang A, Israelsen H, Johnsen MG, Bredmose L;

PI Arnau J;

XX

PCR primer used to
PCR primer used to
M catarrhalis MCAL
Novel Helicobacter
Staphylococcus aur
Human G-protein co
Nitrophenyl phosph
Antisense primer u
Locked nucleoside
Human RGS9 related
Mutant pACYC184 pl
Human nuclear rece
Methanococcus jann
Human CLCA1 gene e
Primer KS4. Synth
SREBP probe #4. S
Novel Helicobacter
Primer #4 related
mrp gene promoter,
Physiologically ac
5' PCR primer used
Methanococcus jann
Vitamin D 24 hydro
Novel Helicobacter
Human motor protei
Human interferon-g
PEA toxin gene and
Transformed lympho
End-locked five-he
PCR primer for tet
M30 protein vector
Activated T-cell d
Human PMWP protein
Neisseria meningit
PCR primer for kno
Human CLCA1 gene e

DR WPI; 2001-191547/19.

XX Constructing a transposon derivative to identify DNA sequence encoding

PT signal peptide in lactic acid bacteria, involves removing stop codons

PT in frame with secretion reporter molecule from DNA comprising

PT transposon -

XX

XX Example 1; Page 14; 62pp; English.

XX The present invention describes a method for constructing a transposon

CC derivative for identifying DNA (I) encoding a signal peptide (secretion

CC signal, SP) in a lactic acid bacterium (e.g. *Lactococcus lactis*). The

CC method comprises selecting a transposon (II), including a promoterless

CC promoter reporter (PPR) gene and a ribosome binding site (RBS), between

CC its left and right termini (LR) and (RR), deleting a region between LR

CC and PPR gene to obtain modified DNA that retains its transposability and

CC its RBS. The present invention also describes: (i) a transposon

CC derivative (III) for the identification of (I) in a lactic acid

CC bacterium, comprising (II) without stop codons in the region upstream of

CC the PPR gene, and a DNA sequence encoding a secretion reporter molecule

CC without a sequence coding for SP; (2) an isolated DNA molecule (IV)

CC comprising at least a part of (III) and (I) that is functional in a

CC lactic acid bacterium; (3) an isolated DNA sequence (I) coding for SP

CC derived from SP10, SP13, SP307, SP310 or SP330, or a derivative of any of

CC the signal peptides having retained signal peptide functionality; (4) a

CC recombinant plasmid (V) comprising (II) or (I); and (5) a recombinant

CC bacterium (VI) comprising (I). (III) is useful for identifying and

CC isolating (I) from a source lactic acid bacteria, by transforming the

CC bacteria with (III), and selecting from the transformed bacteria, cells

CC in which the promoterless promoter reporter gene is expressed and the

CC gene product of the DNA sequence coding for a secretion reporter molecule

CC is secreted. (VI) is useful for the production of a desired gene product.

CC AAF59460 to AAF59499 and AAB70428 to AAB70472 represent sequences used

CC in the exemplification of the present invention.

XX

SQ Sequence 38 BP; 14 A; 8 C; 7 G; 9 T; 0 other;

Query Match 1.1%; Score 20.6; DB 22; Length 38;

Best Local Similarity 85.2%; Pred. No. 8.5e+04;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1475 ACTTTCATCATTTTTCATCGTATTCGT 1501

||||| ||||| ||||| ||||| |||||

Db 35 ACTTTTATATTTTATAGATCGAATTCGT 9

RESULT 2

AAx91515/c

ID AAX91515 standard; DNA; 33 BP.

XX

AC AAX91515;

XX

DT 28-SEP-1999 (first entry)

XX

DE Bovine interferon-alpha gene amplifying primer aIFNsrev.

XX

KW Bovine herpes virus-2; BHV-2; cytokine; immune response; immunogen; IL;

KW interleukin; colony stimulating factor; CSF; interferon; IFN; TNF;

KW tumour necrosis factor; recombinant virus; vaccine; mucosal disease;

KW mastitis; breast cancer; stress-induced disease; PCR primer; ss.

XX

OS Synthetic.

OS Bos sp.

XX

XX WO9916892-A1.

PN

XX

PD 08-APR-1999.

XX

PF 29-SEP-1998; 98WO-GB02927.

XX

PR 29-SEP-1997; 97GB-0020633.

XX

XX (UYBR-) UNIV BRISTOL.

PA

XX Bradley AJ, Duffas WPH;

XX WPI; 1999-255101/21.

DR

XX New bovine herpes virus-2 vectors

PT

XX

XX Example 2; Page 34; 130pp; English.

XX The invention provides bovine herpes virus-2 (BHV-2) based vectors that

CC comprise at least one cytokine-encoding DNA sequence. The expression of

CC cytokines in mammals can up-regulate immune responses to the immunogens.

CC The cytokine is selected from interleukins (IL), colony stimulating

CC factors (CSF), interferons (IFN) and tumour necrosis factors (TNF). The

CC BHV-2 based vector or recombinant virus can be used as vaccines. They can

CC be used for preventing or treating a mucosal disease in a subject, e.g.

CC ruminants, cattle, sheep, goats, dogs, cats, horses, or man, particularly

CC mastitis in cows or breast cancers in humans. They can also be used for

CC preventing or treating a stress-induced disease.

XX

SQ Sequence 33 BP; 10 A; 8 C; 9 G; 6 T; 0 other;

Query Match 1.1%; Score 20.4; DB 20; Length 33;

Best Local Similarity 80.0%; Pred. No. 9.1e+04;

Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 862 TGCTCTCGGTTTGAGCTGCGAATTCGCT 891

||||| ||||| ||||| ||||| |||||

Db 33 TGCTCTCGGTTTGACCTGCGAATTCAGT 4

RESULT 3

AAx43955/c

ID AAS43955 standard; DNA; 34 BP.

XX

AC AAS43955;

XX

DT 18-DEC-2001 (first entry)

XX

DE *Neisseria meningitidis* B MC58 genomic DNA sequence PCR primer #50.

XX

KW *Neisseria gonorrhoeae*; leader peptide; fusion protein; ORF46.1; ss;

KW *Neisseria* protein; PCR primer.

XX

OS *Neisseria meningitidis*.

OS Synthetic.

XX

XX WO200164922-A2.

PN

XX

PD 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-IB00452.

XX

PR 28-FEB-2000; 2000GB-0004695.

XX

PR 13-NOV-2000; 2000GB-0027675.

XX

PA (CHIR-) CHIRON SPA.

XX

XX Arico MB, Comanducci M, Galeotti C, Masignani V, Guilianini MM;

PI Pizza M;

XX

XX WPI; 2001-582163/65.

DR

XX Producing heterologous proteins from *Neisseria meningitidis* and *N.*

PT *gonorrhoeae* -

XX

XX Disclosure; Page 82; 119pp; English.

XX The invention relates to methods for the heterologous expression of

CC *Neisseria* proteins from *Neisseria meningitidis* and *Neisseria*

CC *gonorrhoeae*. At least one domain in the protein is deleted, e.g. the

CC leader peptide, and may be replaced by a domain from a different protein

CC to make a fusion protein, in order to enhance heterologous expression of

XX ABZ25344;
AC
XX 21-MAR-2003 (first entry)
DT
XX PCR primer MYK107, SEQ ID 30.
DE
XX Antiparkinsonian; neuroprotective; nerve cell transmission; brain;
KW nervous system; Parkinson's disease; PCR; primer; ss.
KW
XX Synthetic.
OS
XX WO200286131-A1.
PN
XX 31-OCT-2002.
PD
XX 09-APR-2002; 2002WO-JP03537.
PF
XX 09-APR-2001; 2001JP-0109445.
PR
XX (GENC-) GENCOM CORP.
PA
XX Yamamoto M, Watanabe D, Teranishi Y, Nakanishi S;
PI WPI; 2003-103413/09.
DR
XX Gene unit for reversible control of expression of a protein regulating
PT nerve cell transmission function in specific nerve cells and transgenic
PT animals incorporating it for analysis of the biology and functional
PT mechanisms of nerve cells -
XX
XX Example 2; Page 86; 93pp; Japanese.
PS
XX The present invention relates to a gene expression control unit which
CC contains: (a) a DNA sequence which reversibly controls the expression of
CC a protein having nerve cell transmission function control activity; and
CC (b) DNA encoding the protein under the control of (a). The invention is
CC useful as models for the study of the brain nerve system network and for
CC investigation of methods for the treatment and diagnosis of brain and
CC nerve diseases including Parkinson's disease and the effects of drug
CC administration. The present sequence is a PCR primer, which was used in
CC an example from the invention.
XX
XX Sequence 40 BP; 7 A; 11 C; 8 G; 14 T; 0 other;
SQ
Query Match 1.1%; Score 20.4; DB 25; Length 40;
Best Local Similarity 71.1%; Pred. No. 9.8e+04;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 545 TCTGTAGAAAAGGATATACCAAGGCTTTTGGAGCCAT 582
DB 40 TCATTAGATAAAGGATACATAAAGCGCGCGCAGCCAT 3
RESULT 7
AA97008/c
ID AAX97008 standard; DNA; 20 BP.
AC
XX AAX97008;
AC
XX 13-SEP-1999 (first entry)
DT
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
DE
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
KW
XX Synthetic.
OS
XX Chlamydia pneumoniae.
OS
XX WO9927105-A2.
PN
XX

PD 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB01890.
PF
XX 04-NOV-1998; 98US-0107078.
PR
XX 21-NOV-1997; 97FR-0014673.
PR
XX (GEST) GENSET.
PA
XX Griffais R;
PI
XX WPI; 1999-357842/30.
DR
XX Genome sequence of Chlamydia pneumoniae
XX
XX Page 1870; Disclosure; 1912pp; English.
PS
XX AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAX94584-
CC AAX35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotides sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 other;
SQ
Query Match 1.1%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.4e+04; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 54 ATTCTGCAAAACCGTGGATGG 73
DB 20 ATTCTGCAAAACCGTGGATGG 1
RESULT 8
AA95807
ID AAX95807 standard; DNA; 20 BP.
AC
XX AAX95807;
AC
XX 13-SEP-1999 (first entry)
DT
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
DE
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
KW
XX Synthetic.
OS
XX Chlamydia pneumoniae.
OS
XX WO9927105-A2.
PN
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-IB01890.
PF
XX 04-NOV-1998; 98US-0107078.
PR
XX 21-NOV-1997; 97FR-0014673.
PR
XX (GEST) GENSET.
PA
XX Griffais R;
PI
XX WPI; 1999-357842/30.
DR
XX Genome sequence of Chlamydia pneumoniae
XX
XX

ID AAL46489 standard; DNA; 40 BP.
 AC AAL46489;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE M catarrhalis MCA101924 gene PCR primer #1.
 XX
 KW Moraxella; vaccine; respiratory tract infection; antiinflammatory;
 KW auditory; antibacterial; otitis media; sinusitis; pneumonia; PCR;
 KW primer; ss.
 XX
 OS Moraxella catarrhalis.
 XX
 XX WO200218595-A2.
 XX
 PD 07-MAR-2002.
 XX
 XX 28-AUG-2001; 2001WO-CA01321.
 XX
 PR 28-AUG-2000; 2000US-228294P.
 PR 28-AUG-2000; 2000US-228295P.
 PR 28-AUG-2000; 2000US-228296P.
 PR 29-AUG-2000; 2000US-228438P.
 PR 29-AUG-2000; 2000US-228439P.
 PR 29-AUG-2000; 2000US-228440P.
 PR 29-AUG-2000; 2000US-228441P.
 PR 29-AUG-2000; 2000US-228442P.
 PR 29-AUG-2000; 2000US-228443P.
 PR 29-AUG-2000; 2000US-228511P.
 PR 29-AUG-2000; 2000US-228512P.
 PR 29-AUG-2000; 2000US-228742P.
 PR 29-AUG-2000; 2000US-228773P.
 PR 01-SEP-2000; 2000US-229465P.
 PR 01-SEP-2000; 2000US-229474P.
 PR 01-SEP-2000; 2000US-229475P.
 PR 01-SEP-2000; 2000US-229478P.
 PR 05-SEP-2000; 2000US-229740P.
 PR 05-SEP-2000; 2000US-229803P.
 PR 05-SEP-2000; 2000US-229804P.
 PR 05-SEP-2000; 2000US-229805P.
 PR 05-SEP-2000; 2000US-229806P.
 PR 05-SEP-2000; 2000US-229811P.
 PR 06-SEP-2000; 2000US-230214P.
 PR 06-SEP-2000; 2000US-230250P.
 PR 06-SEP-2000; 2000US-230252P.
 XX
 XX (AVET) AVENTIS PASTEUR LTD.
 XX
 XX Loosmore S, Wang J, Bradley B, Ochs M, Yang Y;
 XX WPI; 2002-401721/43.
 XX
 XX Moraxella polypeptide and polynucleotides useful as vaccine for
 PT immunizing a host e.g. humans against disease e.g. otitis media,
 PT pneumonia, caused by infection of the bacteria
 XX
 XX Example 1; Page 73; 277pp; English.
 XX
 CC The present invention provides the protein and coding sequences of
 CC proteins from Moraxella catarrhalis. These can be used to produce
 CC vaccines which protect against M. catarrhalis infection, which can cause
 CC otitis media, respiratory infection, sinusitis, and pneumonia. The
 CC present sequence is a PCR primer used to isolate a coding sequence of
 CC the invention.
 XX
 XX Sequence 40 BP; 6 A; 2 C; 14 G; 18 T; 0 other;
 SQ
 Query Match 1.1%; Score 19.8; DB 24; Length 40;
 Best Local Similarity 77.4%; Pred. No. 1.4e+05;
 Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 310 GGCAATGCTTATTGTTTGTGATGAGCGTATAT 340
 DB 1 GGAATTTCATATGTTTGTGATGAGTGTGTTT 31
 RESULT 12
 ABX67554
 ID ABX67554 standard; DNA; 30 BP.
 XX
 AC ABX67554;
 XX
 DT 07-MAY-2003 (first entry)
 XX
 DE Novel Helicobacter pylori gene PCR primer #525.
 XX
 KW Protein-protein interaction; ulcer; selected interacting domain;
 KW SID; PCR; primer; ss.
 XX
 OS Helicobacter pylori.
 XX
 XX WO200266501-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 28-DEC-2001; 2001WO-EP15428.
 XX
 XX 02-JAN-2001; 2001US-259302P.
 XX
 XX (HYBR-) HYBRIGENICS.
 XX (INSP) INST PASTEUR.
 XX
 XX Legrain P, Rain J, Colland F, De Reuse H, Labigne A;
 XX WPI; 2002-674910/72.
 XX
 PT New complexes of protein-protein interactions in Helicobacter pylori,
 PT useful for identifying modulating compounds for treating or preventing
 PT ulcers in mammals -
 XX
 XX Example 9; Page 504; 642pp; English.
 XX
 CC The invention describes a complex of protein-protein interactions in
 CC Helicobacter pylori selected from 421 complexes given in the
 CC specification. The complex of protein-protein interactions are useful
 CC for screening for agents which modulate the interaction of proteins.
 CC Modulating compounds which binds to a targeted bacterial protein may be
 CC used for treating or preventing ulcers in a human or animal. This
 CC sequence represents a primer used to isolate polynucleotides encoding
 CC Helicobacter pylori proteins for studies on protein-protein
 CC interactions.
 XX
 XX Sequence 30 BP; 6 A; 4 C; 4 G; 13 T; 3 U; 0 other;
 SQ
 Query Match 1.1%; Score 19.6; DB 24; Length 30;
 Best Local Similarity 80.8%; Pred. No. 1.4e+05;
 Matches 21; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1603 ATCAGTTTGTATGCTTTGTTTGA 1628
 DB 5 AUCAUTTGTGTTTAAATGCGTTGTTTA 30
 RESULT 13
 AAZ21084/c
 ID AAZ21084 standard; DNA; 32 BP.
 XX
 AC AAZ21084;
 XX
 DT 17-NOV-1999 (first entry)
 XX
 DE Staphylococcus aureus trxB PCR primer #1.
 XX
 KW Staphylococcus; trxB; thioredoxin reductase; antimicrobial;

KW PCR primer; ss.
 XX Synthetic.
 OS Staphylococcus aureus.
 XX WO9945123-A1.
 PN 10-SEP-1999.
 XX 02-MAR-1999; 99WO-US04512.
 XX 02-MAR-1998; 98US-0076525.
 PR (ABBO) ABBOTT LAB.
 XX Aharonowitz Y, Borovok I, Cohen G, Uziel O, Katz L;
 DR WPI; 1999-551044/46.
 XX A new thioredoxin reductase from Staphylococcus aureus -
 PT Example 3; Page 32; 59pp; English.
 PS The present invention describes Staphylococcus thioredoxin reductase
 CC (TrxB). The present sequence represent a PCR primer for S. aureus TrxB.
 CC TrxB inhibitors can be used as antimicrobials to treat a Staphylococcus,
 CC particularly S. aureus, infection. TrxB inhibitors are antimicrobials to
 CC which, unlike most of those in the prior art, Staphylococcus has not yet
 CC developed a resistance.
 XX Sequence 32 BP; 11 A; 3 C; 7 G; 11 T; 0 other;
 SQ Query Match 1.0%; Score 19.4; DB 20; Length 32;
 Best Local Similarity 79.3%; Pred. No. 1.7e+05;
 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1055 ATCAAAATCTATTTAGTGATTAAGCTTT 1083
 DB 32 ATCAAAATCTATTTAGTGATTAAGCTTT 4
 RESULT 14
 ABQ81130
 ID ABQ81130 standard; DNA; 32 BP.
 AC ABQ81130;
 XX 25-NOV-2002 (first entry)
 DT Human G-protein coupled receptor GPR54 PCR primer HGPR54.R8.
 DE GPR54; G-protein coupled receptor; receptor; human; gene therapy;
 KW antidiabetic; analgesic, vasotropic; antimigraine; antidepressant;
 KW nootropic; neuroprotective; tranquilizer; PCR; primer; ss.
 XX Homo sapiens.
 OS WO200259344-A2.
 PN 01-AUG-2002.
 XX 14-DEC-2001; 2001WO-US48333.
 PF 18-DEC-2000; 2000US-256299P.
 PR (MERI) MERCK & CO INC.
 PA Liu Q, Clements M, McDonald TP;
 PI WPI; 2002-666905/71.
 XX New isolated GPR54 polynucleotides and polypeptides, useful for
 PT preventing and/or treating disorders associated with an excess or

PT deficiency of GPR54 protein, such as diabetes, pain, anxiety,
 PT depression and Alzheimer's disease -
 XX Example 1; Page 77; 125pp; English.
 PS The present sequence is that of PCR primer HGPR54.R8, which was
 CC used with primer HGPR54.F6 (see ABQ81129) in a second-round PCR
 CC for the amplification of human G-protein coupled receptor GPR54
 CC cDNA. The template was a first-round PCR (see ABQ81127-28)
 CC product. A clone containing a full-length GPR54 coding sequence
 CC (see ABQ81125) was obtained. The invention provides human and
 CC mouse GPR54 polypeptides and polynucleotides, and methods of
 CC inhibiting or activating these polypeptides and polynucleotides for
 CC use in preventing and/or treating abnormal conditions associated
 CC with excess or insufficient human GPR54 activity, such as eating
 CC disorders, diabetes, pain, migraine, anxiety, depression, ischaemia,
 CC Alzheimer's disease, and reproductive and sleep disorders.
 XX Sequence 32 BP; 12 A; 7 C; 5 G; 8 T; 0 other;
 SQ Query Match 1.0%; Score 19.4; DB 24; Length 32;
 Best Local Similarity 79.3%; Pred. No. 1.7e+05;
 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1038 TTGGATCTTCAGAAAGATCAAAATCTAT 1066
 DB 4 TTGGATCTTCAGAGACCAAAATATTT 32
 RESULT 15
 AAH75604/c
 ID AAH75604 standard; DNA; 33 BP.
 XX AC AAH75604;
 XX 26-OCT-2001 (first entry)
 DT Human withering related protein 22 PCR primer 5.
 DE Human; cell withering related protein 22; malignant tumour; nosohaemia;
 KW human immunodeficiency virus; HIV; infection; immunological disease;
 KW inflammation; PCR primer; ss.
 XX Homo sapiens.
 OS CN1297906-A.
 PN 06-JUN-2001.
 XX 24-NOV-1999; 99CN-0124099.
 PF 24-NOV-1999; 99CN-0124099.
 PR (SHAN-) SHANGHAI BORONG GEGENE DEV CO LTD.
 PA Mao Y, Xie Y;
 PI WPI; 2001-489652/54.
 DR Human cell withering related protein 22 and encoding polynucleotides,
 PT useful for treating tumour, human immunodeficiency virus infection and
 PT inflammation -
 XX Example 5; Page 18 Disclosure; 27pp; Chinese.
 PS The invention relates to the human cell withering related protein 22. The
 CC polypeptide is useful for treating various diseases, such as malignant
 CC tumour, nosohaemia, human immunodeficiency virus (HIV) infection,
 CC immunological diseases and inflammations. The present sequence is a that
 CC of the human cell withering related protein 22 PCR primer.
 CC Note: The present sequence given as SEQ ID NO 5 in the examples differs
 CC from that given as SEQ ID NO 5 in the sequence listing (AAH75602).
 XX

SQ Sequence 33 BP; 14 A; 6 C; 7 G; 6 T; 0 other;
Query Match 1.0%; Score 19.4; DB 22; Length 33;
Best Local Similarity 79.3%; Pred. No. 1.7e+05;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 614 TCAGCACTCTTTCTTCTCTAGATACAGG 642
DB 29 TCAGCTTTCTTTCTTCATGATCCGG 1

RESULT 16
ABQ82518
ID ABQ82518 standard; DNA; 35 BP.
XX
AC ABQ82518;
DT 18-DEC-2002 (first entry)
XX
DE Nitrophenyl phosphatase gene PCR primer AP7R1 SEQ ID NO:28.
XX
KW Promoter; stationary phase-specific promoter; Gram-negative bacteria;
KW expression; protein synthesis; biotechnological; nitrophenyl phosphatase;
KW PCR primer; ss.
XX
OS Aeropyrum pernix.
OS Synthetic.
XX
PN WO200272819-A1.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP02341.
XX
PR 14-MAR-2001; 2001JP-0072802.
XX
PA (TAKA-) TAKARA BIO INC.
XX
PI Shimojo T, Takakura H, Ochiai K, Asada K, Kato I;
XX
DR WPI; 2002-723352/78.
XX
PT Promoters for expression of target gene products, applicable in protein
PT synthesis by biotechnological methods -
XX
PS Example 5; Page 45; 54pp; Japanese.
XX
CC The present invention describes an isolated DNA comprising: (a) an
CC isolated DNA containing a DNA with a base sequence of any of the defined
CC sequences (i)-(vi) given in ABQ82491 to ABQ82496, or their fragments, and
CC showing a stationary phase-specific promoter activity in Gram-negative
CC bacteria; and (b) an isolated DNA hybridizable with the DNA in (a) under
CC stringent conditions. Also described: (i) a recombinant DNA containing
CC the DNA and a foreign gene in which the DNA is so placed as to enable
CC expression of the foreign gene; (ii) an expression vector for expressing
CC a gene that contains the DNA; (iii) a transformant cell that can sustain
CC the recombinant DNA, or expression vector; (iv) a process for producing
CC a protein by culturing the transformant cells and collecting the product
CC from the cultured material; and (v) a kit for the protein production
CC containing the DNA, or the vector for expressing the gene. The promoters
CC are applicable in protein synthesis by biotechnological methods. With
CC these promoters, gene products can be conveniently obtained with high
CC expression, at low cost. The present sequence represents a PCR primer
CC for nitrophenyl phosphatase, which is used in an example from the present
CC invention.
XX
SQ Sequence 35 BP; 6 A; 14 C; 10 G; 5 T; 0 other;
Query Match 1.0%; Score 19.2; DB 24; Length 35;
Best Local Similarity 75.0%; Pred. No. 2e+05;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 418 GGATGCCCACTCCTCTGTGAGACTCGCTG 449

DB 3 GGACGGCTCACCCCTCTGTCAGAACTCGTG 34
RESULT 17
AAX26795/c
ID AAX26795 standard; DNA; 27 BP.
XX
AC AAX26795;
XX
DT 21-JUN-1999 (first entry)
XX
DE Antisense primer used to amplify exon 1 of human k-ras nucleic acids.
XX
KW Human k-ra; fluorescent nucleoside conjugate; ribo-nucleoside;
KW fluorescent marker; rare earth cryptate; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /note= "biotinylated"
XX
PN FR2769315-A1.
XX
PD 09-APR-1999.
XX
PF 03-OCT-1997; 97FR-0012379.
XX
PR 03-OCT-1997; 97FR-0012379.
XX
PA (CISB-) CIS BIO INT SA.
XX
PI Bazin H, Mathis G;
XX
DR WPI; 1999-246944/21.
XX
PT Fluorescent nucleoside and nucleotide conjugates containing a rare
PT earth cryptate
XX
PS Example 3; Page 14; 30pp; French.
XX
CC PCR primers AAX26794-95 were used to amplify exon 1 of human k-ras
CC nucleic acids. The specification describes fluorescent nucleoside
CC and nucleotide conjugates comprising a ribo- or deoxyribo-nucleoside
CC or nucleotide (natural, modified, or conjugated to a marker), of which
CC at least one puric or pyrimidinic ring C atom or exocyclic N atom may
CC be linked to a bond with a fluorescent marker, and at least one rare
CC earth cryptate as fluorescent marker attached to this atom. The
CC fluorescent nucleoside and nucleotide conjugates can be used as
CC markers, as nucleotides in nucleic acid syntheses, for the detection
CC and localization of compounds containing at least one nucleic sequence,
CC to measure the enzymatic activity of an enzyme used in nucleic
CC acid syntheses, particularly polymerase, inverse transcriptase,
CC transferase, or ligase, and to measure the enzymatic activity of a
CC nucleic acid substrate.
XX
SQ Sequence 27 BP; 8 A; 5 C; 5 G; 9 T; 0 other;
Query Match 1.0%; Score 19; DB 20; Length 27;
Best Local Similarity 81.5%; Pred. No. 2e+05;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 727 CATGCTGGATGAATAAGACCCCAACA 753
DB 27 CATTTGTGGACGAATATGATCCAACA 1
RESULT 18
AAX56490/c
ID AAX56490 standard; DNA; 35 BP.

XX AAX56490;
 XX 27-JUL-1999 (first entry)
 XX Locked nucleoside analogue oligomer ODN#10.
 XX Locked nucleoside analogue; LNA; bicyclic; tricyclic; diagnosis;
 KW PCR application; strand displacement oligomer; polymerase; substrate;
 KW nucleotide based drug; diagnostic probe; antisense therapy;
 KW antiviral; antitumour; ss.
 XX Synthetic.
 OS
 XX WO9914226-A2.
 PN
 XX 25-MAR-1999.
 PD
 XX 14-SEP-1998; 98WO-DK00393.
 XX 28-JUL-1998; 98DK-0000982.
 XX 12-SEP-1997; 97DK-0001054.
 PR 19-DEC-1997; 97DK-0001492.
 PR 16-JAN-1998; 98DK-0000061.
 PR 03-MAR-1998; 98DK-0000286.
 PR 29-APR-1998; 98DK-0000585.
 PR 05-JUN-1998; 98US-0088309.
 PR 08-JUN-1998; 98DK-0000750.
 XX (EXIQ-) EXIQON AS.
 PA
 XX Nielsen P, Wengel J;
 PI
 XX WPI; 1999-337376/28.
 DR
 XX New oligonucleotides containing polycyclic, locked nucleoside
 PT analogues, useful e.g. as diagnostic probes or in antisense therapy
 PT
 XX Example 154; Page 175; 269pp; English.
 PS
 XX The present invention describes novel modified oligonucleotides (I)
 CC containing at least one locked nucleoside analog (LNA). Monomeric LNA's
 CC (II) are also described. (I) are used: (i) to bind to target sequences
 CC in double-stranded DNA or RNA (by strand displacement or triplex
 CC formation); (ii) as ribozymes; (iii) as therapeutic antisense, antigenic
 CC or gene activating agents, specifically for recruitment of RNase H; (iv)
 CC diagnostically for isolation, purification, detection, identification,
 CC quantitation or capture of (synthetic) nucleic acid, e.g. as probes or
 CC primers; (v) as aptamers for therapy, diagnosis, RNA-mediated catalytic
 CC processes and for specific binding to antibodies, drugs etc., including
 CC resolution of enantiomers; (vi) for labeling, then separating, cells;
 CC and (vii) to hybridize to non-coding RNA. LNA are used in synthesis of
 CC (I); as therapeutic and diagnostic agents; to equalize the melting point
 CC of unmodified reference oligonucleotides and as enzyme substrates.
 CC Typical therapeutic applications are as antiviral and antitumour agents.
 CC (I) have increased specificity and/or affinity, i.e. higher melting
 CC point (Tm), for complementary RNA or DNA than oligomers not containing
 CC LNA, and are more resistant to nuclease. The present sequence represents
 CC an oligomer used in an example from the present invention.
 XX
 SQ Sequence 35 BP; 5 A; 6 C; 10 G; 14 T; 0 other;
 Query Match 1.0%; Score 19; DB 20; Length 35;
 Best Local Similarity 71.4%; Pred. No. 2.2e+05;
 Matches 25; Conservativity 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1582 AATGACAACAGCTACAACTCTATCAGTTTGTGTTAA 1616
 DB 35 AACTACAACAGCCGCAAGTCCAGCACCTCGTTAA 1
 RESULT 19
 ABN81648/c

ID ABN81648 standard; DNA; 35 BP.
 XX
 AC ABN81648;
 XX
 DT 29-AUG-2002 (first entry)
 XX
 DE Human RGS9 related PCR primer SEQ ID NO 25.
 XX
 KW RGS; regulator of G-proteins; pheromone; luciferase; Renilla; Photinus;
 KW GFP; high through-put screening; human; RGS9; PCR; primer; ss.
 XX
 OS Synthetic.
 XX WO200250104-A2.
 PN
 XX 27-JUN-2002.
 PD
 XX 03-DEC-2001; 2001WO-US45105.
 PF
 XX 01-DEC-2000; 2000US-250147P.
 PR
 XX (AMHP) AMERICAN HOME PROD CORP.
 PA
 XX Young KH, Cao J, Sheu Y D;
 PI
 XX WPI; 2002-500622/53.
 DR
 XX Novel cell for detecting ability of test sample to alter RGS
 PT protein-mediated reporter gene expression, comprises a heterologous
 PT nucleic acid encoding reporter operably linked to pheromone-responsive
 PT promoter -
 PT
 XX Example 7; Page 31; 95pp; English.
 PS
 XX The invention relates to a cell (I) that responds to a pheromone
 CC comprising a heterologous nucleic acid encoding a reporter operably
 CC linked to a pheromone-responsive promoter (the reporter is Renilla
 CC luciferase, Photinus luciferase, green fluorescent protein (GFP) or its
 CC derivative or a heterologous nucleic acid encoding chimeric regulator of
 CC G-protein (RGS protein)). (I) is useful for detecting the ability of a
 CC test sample to alter RGS protein-mediated reporter gene expression,
 CC by: (a) providing (I) where expression of heterologous nucleic acid
 CC molecule produces a measurable signal, providing another cell similar to
 CC (I) further comprising a second heterologous nucleic acid encoding an RGS
 CC protein, incubating a test sample with the cells in the presence of a
 CC pheromone under conditions suitable to detect the measurable signal,
 CC detecting the level of expression of the heterologous nucleic acid,
 CC encoding the reporter and comparing the level of expression of the
 CC reporter in the first and second cells, where a difference in the level
 CC of expression indicates that the test sample alters RGS protein-mediated
 CC reporter gene expression; or (b) providing two aliquots of (I),
 CC incubating the aliquots of cells in the presence of a pheromone under
 CC conditions suitable to detect the measurable signal, where one of the
 CC aliquots contains a test sample, detecting the level of expression of the
 CC heterologous nucleic acid encoding the reporter in the aliquots and
 CC comparing the level of expression of the reporter in the aliquots, where
 CC a difference in the level of expression between the aliquots indicates
 CC that the test sample alters RGS protein-mediated reporter gene
 CC expression. The test sample used is at a single concentration or in the
 CC range of concentrations. The expression of reporter gene is detected in a
 CC halo assay, detected spectrometrically or the detection is automated.
 CC Since the method of detecting the ability of test sample to modulate RGS
 CC mediated reporter gene expression using (I) can be automated, the method
 CC can be used for screening test compounds on a large scale. The method is
 CC sensitive, can be carried out within a short test period, and is ideal
 CC for high through-put systems used in large scale drug discovery. The
 CC present sequence is that of a PCR primer used to generate constructs for
 CC testing the functional complementation of mammalian RGS proteins in
 CC examples of the invention.
 XX
 SQ Sequence 35 BP; 11 A; 13 C; 8 G; 3 T; 0 other;
 Query Match 1.0%; Score 19; DB 24; Length 35;

Best Local Similarity 71.4%; Pred. No. 2.2e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1134 GCTGGCGTTATTGGGATTGTGTGAGAACAGG 1168
|||||
Db 35 GCTGGCGTTGTGCGGATTGTATCTGGATCCGG 1

RESULT 20
AAZ46427
ID AAZ46427 standard; DNA; 31 BP.
XX AC AAZ46427;
XX DT 06-MAR-2000 (first entry)
XX DE Mutant pACYC184 plasmid constructing linker 184delTet-2.
XX XX Mutational vector; genetic change; therapeutic; mutant; linker; ss.
XX OS Synthetic.
XX PN W0958723-A1.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US10514.
XX PR 12-MAY-1998; 98US-0078063.
XX PA (KIME-) KIMERAGEN INC.
XX PI Kumar R, Metz RA;
XX XX WPI; 2000-062307/05.
XX XX New mutational vectors, used to introduce specific genetic changes in target DNA sequences in prokaryotic and eukaryotic cells or episomes - Examples; Page 13; 37pp; English.
XX CC The invention relates to new mutational vectors that contains a nucleobase strand which alters the sequence of DNA in target cells. The mutational vectors can be used to introduce specific genetic changes in target DNA sequences in prokaryotic and eukaryotic cells or episomes. Such changes can be used to create new phenotypic traits not found in nature, in a subject as a therapeutic or prophylactic intervention and as an investigational tool. Sequences AAZ46426-427 represent linkers replacing a deleted tetracycline region of pACYC184.
XX XX Sequence 31 BP; 6 A; 7 C; 8 G; 10 T; 0 other;
SQ

Query Match 1.0%; Score 18.8; DB 21; Length 31;
Best Local Similarity 76.7%; Pred. No. 2.4e+05;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 852 TAGGTTGCGTTGCTCTCGGTTTGGAGCCT 881
|||||
Db 2 TAGGTTTCACTGCATCTCGAGATTGGATCCT 31

RESULT 21
AAC67280/c
ID AAC67280 standard; DNA; 33 BP.
XX AC AAC67280;
XX DT 09-APR-2001 (first entry)
XX DE Human nuclear receptor NOT1 DNA response element.
XX XX Human; nuclear receptor; NOT1; splice variant; neurological disease; immune disease; cancer; cardiovascular disease; ds.
KW

XX OS Homo sapiens.
XX PN W0200077202-A1.
XX PD 21-DEC-2000.
XX XX 14-JUN-2000; 2000WO-GB02317.
XX XX 15-JUN-1999; 99GB-0013863.
XX XX (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Kremer A, Jackson AR, Cairns WJ;
XX DR WPI; 2001-071271/08.
XX XX Nuclear receptor NOT1 splice variant polypeptide, useful for treating metabolic disorders, cancer, neurological and immune disorders and for identifying agonists/antagonists useful in therapy - Example 1; Page 22; 37pp; English.
XX CC The present invention provides the protein and coding sequences of the human nuclear receptor NOT1 splice variant NOT1A. The NOT1A protein is involved in the control of gene expression and the sequences can be used in the treatment of cancer, neurological and immune disorders and cardiovascular disease.
XX XX Sequence 33 BP; 10 A; 8 C; 9 G; 6 T; 0 other;
SQ

Query Match 1.0%; Score 18.8; DB 22; Length 33;
Best Local Similarity 76.7%; Pred. No. 2.4e+05;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1352 ATTCATGACCTTTTGGTACCTGTGCAGTC 1381
|||||
Db 32 ATTCATGACCTTTTGGTACCTGTGCAGTC 3

RESULT 22
AAZ80468/c
ID AAZ80468, standard; DNA; 40 BP.
XX AC AAZ80468;
XX DT 23-AUG-1999 (first entry)
XX DE Methanococcus jannaschii DNA polymerase PCR primer #1.
XX KW Methanococcus jannaschii; DNA polymerase; genetic engineering; PCR primer; ss.
XX OS Synthetic.
XX OS Methanococcus jannaschii.
XX PN JP11151087-A.
XX PD 08-JUN-1999.
XX PF 19-NOV-1997; 97JP-0318665.
XX PR 19-NOV-1997; 97JP-0318665.
XX PA (TAKI) TAKARA SHUZO CO LTD.
XX DR WPI; 1999-388477/33.
XX XX New DNA polymerase gene - useful in genetic engineering
XX XX Example 1; Page 13; 19pp; Japanese.
XX CC The present sequence represents a PCR primer for a Methanococcus

CC jannaschii DNA polymerase. The DNA polymerase gene is useful in the
CC field of gene engineering.

XX
SQ Sequence 40 BP; 19 A; 2 C; 9 G; 10 T; 0 other;
Query Match 1.0%; Score 18.8; DB 20; Length 40;
Best Local Similarity 68.4%; Pred. No. 2.7e+05;
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

XX
SQ Sequence 40 BP; 19 A; 2 C; 9 G; 10 T; 0 other;
Query Match 1.0%; Score 18.8; DB 20; Length 40;
Best Local Similarity 68.4%; Pred. No. 2.7e+05;
Matches 26; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1646 TTTAATTTTGCATTATTATGACCATAGGATTTCTTCT 1683

DB 40 TCTAAGAAATTTATTATTATTCCTCCATATGATATCTCTCT 3

RESULT 23

ABK59400

ID ABK59400 standard; RNA; 37 BP.

XX

AC ABK59400;

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3771.

XX

KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.

XX

OS Homo sapiens.

XX

PN WO200211674-A2.

XX

PD 14-FEB-2002.

XX

PF 09-AUG-2001; 2001WO-US24970.

XX

PR 09-AUG-2000; 2000US-224383P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PA (SYNT) SYNTX USA LLC.

XX

PA (THOM) THOMPSON J.

XX

PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX

PI Grupe A;

XX

PS WPI; 2002-217145/27.

XX

XX Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma

XX Claim 5; Page 95; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down

CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes

CC by cleaving RNA derived from the genes. The nucleic acid sequences are

CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions

CC that are related to or will respond to the levels of CLCA1 in a cell or

CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,

CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises

CC the use of one or more therapies under conditions suitable for the

CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,

CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The

CC nucleic acids of the invention are also used as diagnostic tools to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of CLCA1 RNA in a cell. This sequence represents an

XX enzymatic nucleic acid molecule of the invention.

SQ Sequence 37 BP; 10 A; 6 C; 10 G; 11 U; 0 other;

Query Match 1.0%; Score 18.6; DB 24; Length 37;

Best Local Similarity 45.5%; Pred. No. 2.9e+05;

Matches 15; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

OY 1812 TTTAGTCCCAAGGCCCTGTGGTATTAAATTT 1844

DB 4 UUCAGGCCGAAGGCGAGUGAGGUCUUAACUUU 36

RESULT 24

AAQ31787

ID AAQ31787 standard; DNA; 38 BP.

XX

AC AAQ31787;

XX

DT 25-MAR-2003 (updated)

XX

DT 14-APR-1993 (first entry)

XX

DE Primer KS4.

XX

KW Primer; recombinant DNA; variable domain; light; heavy; chain;
KW antibody; antibody; DI.3; PCR; polymerase chain reaction;
KW bridging; linker; flexible; Fv fragment; ss.

XX Synthetic.

XX

PN WO9220805-A1.

XX

PD 26-NOV-1992.

XX

PF 11-MAY-1992; 92WO-SE00304.

XX

PR 13-MAY-1991; 91SE-0001433.

XX

PA (FABR) FABRE MEDICAMENT SA PIERRE.

XX

PI Hansson M, Nguyen TN, Nygren PA, Stahl S, Uhlen M;

XX

DR WPI; 1992-415783/50.

XX

PT Recombinant DNA encoding staphylococcal proteins - useful for
PT isolation and identification of Gram positive bacteria and in
PT vaccines

XX

PS Disclosure; Page 8; 30pp; English.

XX

CC The sequences given in AAQ31784-89 are primers which were used in the
CC construction of a recombinant DNA sequence containing the two
CC variable domains of the light and heavy chains of the anti-lysozyme
CC antibody DI.3. The two variable regions were then linked by PCR via
CC a 15 amino acid bridging linker which was highly flexible. The
CC resulting amplification product was a 730 bp gene fragment encoding
CC a single chain Fv fragment of DI.3, represented by:
CC NH2-VL-linker-VH-COOH.

CC (Updated, on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 38 BP; 6 A; 9 C; 9 G; 14 T; 0 other;

XX

Query Match 1.0%; Score 18.6; DB 13; Length 38;

Best Local Similarity 72.7%; Pred. No. 2.9e+05;

Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 848 CTTTAGGTTGGTCTCTCGGTTTGAGCC 880

DB 6 CTTTATAGATCCTTTGATTTCCAGCTTGTCGCC 38

RESULT 25

AAQ79013/c

ID AAQ79013 standard; DNA; 38 BP.

XX

XX WPI; 2002-106611/14.
 XX New human semaphorin protein 9 for diagnosing and treating nervous
 PT system deforming and disease associated with functional disturbance of
 PT the nervous system -
 XX Example 5; Page 13; 37pp; Chinese.
 XX This invention relates to an isolated polypeptide of human semaphorin
 CC protein 9, thought to be neurotropic and neuroprotective in its
 CC action. The proteins and encoding sequences are used in diagnosis and
 CC treatment of nervous system deforming and disease associated with
 CC functional disturbance of the nervous system. This sequence
 CC represents a primer related to semaphorin protein 9.
 XX Sequence 33 BP; 9 A; 8 C; 3 G; 13 T; 0 other;
 SQ
 Query Match 1.0%; Score 18.4; DB 24; Length 33;
 Best Local Similarity 78.6%; Pred. No. 3.1e+05;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 544 ATCTGTAGAAAGGATATACCAAGGCT 571
 DB ||||||| ||||||| ||||||| ||||||| |||||||
 33 ATGTGTAGTAAAGAAATGTAAGGAT 6
 RESULT 28
 ABS59791
 ID ABS59791 standard; DNA; 34 BP.
 AC ABS59791;
 XX 05-NOV-2002 (first entry)
 DT mrp gene promoter, PCR primer #1.
 XX Streptococcus virulence; iron-restricted induced gene; iri; vaccine;
 KW in vivo selected gene; iva; mrp gene promoter; PCR; primer; ss.
 XX Unidentified.
 OS WO200261070-A2.
 PN 08-AUG-2002.
 PD 31-JAN-2002; 2002WO-NL00073.
 PF 02-FEB-2001; 2001BP-0200419.
 PR (IDLE-) ID-LELYSTAD INST DIERHOUDERIJ EN DIERGEZ.
 PA Smith HE;
 PI WPI; 2002-619248/66.
 DR Modulating the virulence of a Streptococcus for the diagnosis of and
 XX vaccination against streptococcal infections, comprises the
 PT modification of a genomic fragment of Streptococcus suis -
 XX Disclosure; Page 17; 108pp; English.
 XX The invention relates to a method of modulating Streptococcus virulence
 CC by modifying a genomic fragment of it, where the genomic fragment
 CC comprises at least a functional part identifiable by hybridisation in
 CC Streptococcus suis to a nucleic acid or fragment of iron-restricted
 CC induced (iri) or in vivo selected (iva) genes given in the specification,
 CC and obtaining a clone where the genomic fragment has been modified. The
 CC method is useful in modulating the virulence of Streptococcus suis that
 CC may be used in the diagnosis of and vaccination against streptococcal
 CC infections and in the detection of virulence markers of Streptococci. The
 CC vaccine comprising the clone, nucleic acid, vector, or the host cell, is
 CC also useful in the prevention and/or treatment of streptococcal

CC infections. ABS59787-ABS59832 represent Streptococcus suis in vivo
 CC selected (ivs) genes and related PCR primers of the invention.
 XX Sequence 34 BP; 8 A; 5 C; 8 G; 13 T; 0 other;
 SQ
 Query Match 1.0%; Score 18.4; DB 24; Length 34;
 Best Local Similarity 78.6%; Pred. No. 3.2e+05;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 306 GCTTGGCAATGCTATTGTTTGTGATGAG 333
 DB ||||||| ||||||| ||||||| ||||||| |||||||
 6 GCTTGGGAATTCATAATGTTTGTGAG 33
 RESULT 29
 AAT78254/c
 ID AAT78254 standard; DNA; 38 BP.
 XX AAT78254;
 AC 13-OCT-1997 (first entry)
 DT Physiologically active protein p160 Example 9 5'-PCR primer E1008A.
 XX Rho binding activity; protein kinase; protein binding; host cell;
 DE recombinant production; human; polymerase chain reaction; ss.
 KW Synthetic.
 OS JP09135683-A.
 PN 27-MAY-1997.
 PD 25-JUN-1996; 96JP-0184102.
 PF 14-SEP-1995; 95JP-0262553.
 PR (KIRI) KIRIN BREWERY KK.
 PA WPI; 1997-335990/31.
 DR Physiologically active protein p160 - has rho binding activity and
 XX protein kinase activity
 PT Example 9; Page 19; 53pp; Japanese.
 XX The present sequence represents 5'-PCR primer E1008A which is used as
 CC part of a primer pair in Example 9 of the specification about the
 CC physiologically active protein p160. The p160 protein has active Rho
 CC protein-binding and protein kinase activities. The nucleotide sequence
 CC encoding the p160 protein can be put into a vector which can then be
 CC used to transform a host cell. The host cell can be cultured for the
 CC recombinant production of the p160 protein. The p160 protein can be
 CC used in a method to screen for compounds that inhibit the protein
 CC kinase activity.
 XX Sequence 38 BP; 16 A; 6 C; 7 G; 9 T; 0 other;
 SQ
 Query Match 1.0%; Score 18.4; DB 18; Length 38;
 Best Local Similarity 69.4%; Pred. No. 3.3e+05;
 Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 570 CTTTGGAGCATTTTGTGATTCTTAACCTGACTACAG 605
 DB ||||||| ||||||| ||||||| ||||||| |||||||
 36 CTTTTCGATTCTATTCTGCAAGCTTTGTAACAG 1
 RESULT 30
 AAV43417/c
 ID AAV43417 standard; DNA; 38 BP.
 XX AAV43417;
 AC
 XX

DT 27-OCT-1998 (first entry)
 XX 5' PCR primer used in the course of the invention.
 DE protein kinase activity; Rho protein; preparation;
 XX therapeutic composition; PCR primer; ss.
 KW Synthetic.
 OS
 XX JP10191985-A.
 FN
 XX 28-JUL-1998.
 PD
 XX 17-JAN-1997; 97JP-0019870.
 PF
 XX 17-JAN-1997; 97JP-0019870.
 PR
 XX (KIRI) KIRIN BREWERY KK.
 PA
 XX WPI; 1998-460110/40.
 DR
 XX New protein exhibiting protein kinase activity - is not capable of
 PT binding to active Rho protein or its derivative, used, e.g.
 KW therapeutically
 PT
 XX Example 9; Page 20; 60pp; Japanese.
 PS
 XX PCR primers AAV43409-30 are used in the course of the invention. The
 CC specification describes a protein which exhibits protein kinase
 CC activity and is not capable of binding to active Rho protein or its
 CC derivative. The materials may be used for the preparation of
 CC therapeutic compositions.
 CC
 XX Sequence 38 BP; 16 A; 6 C; 7 G; 9 T; 0 other;
 SQ

Query Match 1.0%; Score 18.4; DB 19; Length 38;
 Best Local Similarity 69.4%; Pred. No. 3.3e+05;
 Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 570 CTTTGGACGACATTTTGGATTCTTAACCTGACTACAG 605
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 36 CTTTGGATTATTATGCTGCAAGCTTGTAAACAG 1

RESULT 31
 AAX80470
 ID AAX80470 standard; DNA; 40 BP.
 AC
 XX AAX80470;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Methanococcus jannaschii DNA polymerase PCR primer #3.
 XX
 KW Methanococcus jannaschii; DNA polymerase; genetic engineering;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Methanococcus jannaschii.
 XX
 PN JP11151087-A.
 XX
 PD 08-JUN-1999.
 XX
 XX 19-NOV-1997; 97JP-0318665.
 PF
 XX 19-NOV-1997; 97JP-0318665.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX WPI; 1999-388477/33.
 DR
 XX New DNA polymerase gene - useful in genetic engineering
 PT

XX Example 1; Page 13; 19pp; Japanese.
 PS
 XX The present sequence represents a PCR primer for a Methanococcus
 CC jannaschii DNA polymerase. The DNA polymerase gene is useful in the
 CC field of gene engineering.
 CC
 XX Sequence 40 BP; 9 A; 5 C; 10 G; 16 T; 0 other;
 SQ

Query Match 1.0%; Score 18.4; DB 20; Length 40;
 Best Local Similarity 69.4%; Pred. No. 3.4e+05;
 Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1519 CCTGTTTACCCTCATGCTTTTAGTTAATCATGC 1554
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 CCGATTTAAGCATATGATTGTATGTTCAATGTGC 37

RESULT 32
 AAC60772
 ID AAC60772 standard; DNA; 40 BP.
 XX
 AC AAC60772;
 XX
 DT 06-FEB-2001 (first entry)
 XX
 XX Vitamin D 24 hydroxylase (CYP24) forward PCR primer SEQ ID NO:1.
 DE
 XX Vitamin D 24 hydroxylase; vitamin D receptor; CYP24; VDR; ZNF24;
 KW oncogene; breast cancer; chromosome 20; 20q13.2; PCR primer;
 KW 25-hydroxyvitamin D3 24-hydroxylase enzyme; cytosolic; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200060109-A1.
 PN
 XX 12-OCT-2000.
 PD
 XX 06-MAR-2000; 2000WO-US05972.
 PF
 XX 02-APR-1999; 99US-0285292.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Albertson DG, Pinkel D, Collins C, Gray JW, Ystra B;
 PI
 XX WPI; 2000-656233/63.
 DR
 XX Detecting a predisposition to or a progression of cancer especially
 PT breast cancer in humans comprises detecting levels of Cyp24 in a
 PT biological sample -
 PT
 XX Example 1; Page 53; 73pp; English.
 PS
 XX The present invention describes a method for detecting (I) a
 CC predisposition to cancer in an animal. The method comprises detecting
 CC the level of CYP24 (25-hydroxyvitamin D3 24-hydroxylase enzyme) in a
 CC biological sample from the animal and comparing it with a control sample
 CC taken from a normal, cancer-free tissue, where an increased level of
 CC CYP24 in the biological sample compared to the control sample indicates
 CC a predisposition to cancer in the animal. (I) is useful for detecting a
 CC predisposition to cancer in humans, non-human primates, canines, felines,
 CC murines, bovines, equines, porcines and lagomorphs. An example from the
 CC present invention describes the identification of CYP24 as a driver
 CC oncogene, for amplification at chromosome band 20q13.2; the present
 CC sequence represents a PCR primer for CYP24 which is used in this example.
 CC
 XX Sequence 40 BP; 14 A; 11 C; 8 G; 7 T; 0 other;
 SQ

Query Match 1.0%; Score 18.4; DB 21; Length 40;
 Best Local Similarity 69.4%; Pred. No. 3.4e+05;
 Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

PR 15-JUN-2001; 2001US-0212308.
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
 XX LYamichev V, Allawi H, Dong F, Neri BP, Vener IT;
 PI WPI; 2002-049698/06.
 XX
 XX Identifying oligonucleotides hybridizing to nucleic acids containing
 PT secondary structure, useful in clinical diagnosis, comprises
 PT identifying primers that interact with the target to form an extension
 PT product under amplification conditions.
 XX
 XX Example 18; Fig 54A; 409pp; English.
 XX
 CC The present invention describes a method for identifying oligonucleotides
 CC with desired hybridisation properties to nucleic acid targets containing
 CC secondary structure. The method comprises amplifying a target nucleic
 CC acid having at least one accessible and one inaccessible site. Primers
 CC that form an extension product are identified as the oligonucleotides
 CC which can interact with the folded target nucleic acid. Oligonucleotides
 CC from the present invention can be used in novel detection methods for
 CC clinical diagnostic purposes, including the detection and identification
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 33 BP; 17 A; 0 C; 7 G; 9 T; 0 other;
 Query Match 1.0%; Score 18.2; DB 24; Length 33;
 Best Local Similarity 74.2%; Pred. No. 3.5e+05;
 Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 531 AAGTCTTAAAAAATCTGTAGAAAAAGGATA 561
 DB 2 AAGTTTAAAAAGTTTGAAGTAAAAAGGAGA 32
 RESULT 36
 AAV37858/c
 ID AAV37858 standard; DNA; 36 BP.
 XX
 XX AAV37858;
 XX
 XX 10-SEP-1998 (first entry)
 XX
 DE PEA toxin gene and sfv-Lym PCR primer SEQ ID NO:28.
 XX
 KW Immunotoxin; tumour; HIV antigen; lymphocyte; neuron; cytotoxic cell;
 KW cancer; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9817116-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 23-OCT-1997; 97WO-US19206.
 XX
 PR 23-OCT-1996; 96US-0740003.
 XX
 PA (UYWA-) UNIV WAKE FOREST.
 XX
 PI Chen S;
 XX
 DR WPI; 1998-271753/24.
 XX
 XX Cytotoxic lymphocytes or neurons expressing immunotoxin - useful
 XX for the treatment of cancer or virally-infected cells
 PT
 PT Example 1; Page 45; 82pp; English.
 XX
 XX The present invention represents a PCR primer, from the present
 CC invention, used for amplifying the PEA toxin gene and sfv-Lym.
 CC The present invention describes cytotoxic lymphocytes or neurons
 CC that express and secrete an immunotoxin. The immunotoxin secreted
 CC by the cell is used to kill cancer, especially breast, ovarian,
 CC gastric or brain cancer and virally-infected cells, especially
 CC in HIV infected patients.
 XX
 SQ Sequence 36 BP; 17 A; 0 C; 7 G; 9 T; 0 other;
 Query Match 1.0%; Score 18.2; DB 24; Length 33;
 Best Local Similarity 74.2%; Pred. No. 3.5e+05;
 Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 531 AAGTCTTAAAAAATCTGTAGAAAAAGGATA 561
 DB 2 AAGTTTAAAAAGTTTGAAGTAAAAAGGAGA 32
 RESULT 36
 AAV37858/c
 ID AAV37858 standard; DNA; 36 BP.
 XX
 XX AAV37858;
 XX
 XX 10-SEP-1998 (first entry)
 XX
 DE PEA toxin gene and sfv-Lym PCR primer SEQ ID NO:28.
 XX
 KW Immunotoxin; tumour; HIV antigen; lymphocyte; neuron; cytotoxic cell;
 KW cancer; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9817116-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 23-OCT-1997; 97WO-US19206.
 XX
 PR 23-OCT-1996; 96US-0740003.
 XX
 PA (UYWA-) UNIV WAKE FOREST.
 XX
 PI Chen S;
 XX
 DR WPI; 1998-271753/24.
 XX
 XX Cytotoxic lymphocytes or neurons expressing immunotoxin - useful
 XX for the treatment of cancer or virally-infected cells
 PT
 PT Example 1; Page 45; 82pp; English.
 XX

CC The present sequence represents a PCR primer, from the present
 CC invention, used for amplifying the PEA toxin gene and sfv-Lym.
 CC The present invention describes cytotoxic lymphocytes or neurons
 CC that express and secrete an immunotoxin. The immunotoxin secreted
 CC by the cell is used to kill cancer, especially breast, ovarian,
 CC gastric or brain cancer and virally-infected cells, especially
 CC in HIV infected patients.
 XX
 SQ Sequence 36 BP; 8 A; 10 C; 10 G; 8 T; 0 other;
 Query Match 1.0%; Score 18.2; DB 19; Length 36;
 Best Local Similarity 74.2%; Pred. No. 3.7e+05;
 Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 998 GAAGCTGCTCTTCTCTTAGAGACTTCGGTA 1028
 DB 33 GAAGCTGACGCTCGCTCTAGAGAAATTCGGTA 3
 RESULT 37
 AAV37850/c
 ID AAV37850 standard; DNA; 36 BP.
 XX
 XX AAV37850;
 XX
 XX 10-SEP-1998 (first entry)
 XX
 DE Transformed lymphocyte, MOLT-2Fv23e-PE40, PCR primer SEQ ID NO:20.
 XX
 KW Immunotoxin; tumour; HIV antigen; lymphocyte; neuron; cytotoxic cell;
 KW cancer; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9817116-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 23-OCT-1997; 97WO-US19206.
 XX
 PR 23-OCT-1996; 96US-0740003.
 XX
 PA (UYWA-) UNIV WAKE FOREST.
 XX
 PI Chen S;
 XX
 DR WPI; 1998-271753/24.
 XX
 XX Cytotoxic lymphocytes or neurons expressing immunotoxin - useful
 XX for the treatment of cancer or virally-infected cells
 PT
 PT Example 1; Page 40; 82pp; English.
 XX
 XX The present sequence represents a PCR primer, from the present
 CC invention, used for amplifying the transformed lymphocyte.
 CC MOLT-2Fv23e-PE40. The present invention describes cytotoxic lymphocytes
 CC or neurons that express and secrete an immunotoxin. The immunotoxin
 CC secreted by the cell is used to kill cancer, especially breast,
 CC ovarian, gastric or brain cancer and virally-infected cells,
 CC especially in HIV infected patients.
 XX
 SQ Sequence 36 BP; 8 A; 10 C; 10 G; 8 T; 0 other;
 Query Match 1.0%; Score 18.2; DB 19; Length 36;
 Best Local Similarity 74.2%; Pred. No. 3.7e+05;
 Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 998 GAAGCTGCTCTTCTCTTAGAGACTTCGGTA 1028
 DB 33 GAAGCTGACGCTCGCTCTAGAGAAATTCGGTA 3

RESULT 38
 ABZ58980
 ID ABZ58980 standard; DNA; 39 BP.
 AC
 ABZ58980;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE End-locked five-helix protein gene constructing primer P4.
 XX
 KW Five-helix protein; HIV; gp41; virucide; anti-HIV; vaccine; PCR;
 KW immune response; viral membrane; Ebola viral infection; primer; ss.
 XX
 OS Synthetic.
 XX WO2003006056-A2.
 PN
 XX
 PD 23-JAN-2003.
 XX
 PF 11-JUL-2002; 2002WO-US21915.
 XX
 PR 11-JUL-2001; 2001US-304152P.
 PR 11-JUL-2002; 2002US-0193412.
 XX
 PA (ZHOU/) ZHOU G.
 PI Zhou G;
 PI
 XX
 DR WPI; 2003-221659/21.
 XX
 PT New end-locked five-helix protein comprising 3 N-helices and 2
 PT C-helices of HIV gp41, 4 inside linkers, and at least one terminal
 PT linker, useful for inhibiting HIV infection in a human, and for
 PT eliciting an immune response to HIV in a host -
 XX
 PS Example 1; Page 18; 21pp; English.
 XX
 CC The invention relates to new end-locked five-helix protein comprising 3
 CC N-helices and 2 C-helices of HIV gp41, 4 inside linkers, and at least
 CC one terminal linker. The helices are connected by the inside linker, and
 CC the terminal linker is connected to a helix and is capable of cross-
 CC linking with one of the inside linkers. The end-locked five-helix protein
 CC is useful for inhibiting entry of HIV into a cell, for inhibiting HIV
 CC infection in a human, and for eliciting an immune response to HIV in a
 CC host. The proteins may also be used as fusion inhibitors to block viral
 CC entry or viral membrane fusion, as vaccine (e.g. against Ebola viral
 CC infection), as tools for screening drug candidates against HIV, and as
 CC inhibitors for blocking Ebola viruses. Sequences ABZ58977-988 represent
 CC PCR primers used for constructing the gene encoding the end-locked five-
 CC helix proteins of the invention.
 XX
 SQ Sequence 39 BP; 10 A; 14 C; 4 G; 11 T; 0 other;
 Query Match 1.0%; Score 18.2; DB 25; Length 39;
 Best Local Similarity 74.2%; Pred. No. 3.8e+05;
 Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1587 CAACACCTACACTCTATCAGTTTCTTAAAT 1617
 Db | | | | | | | | | | | | | | | | | | | |
 8 CCACAGCCACCACTCAATAATCTTGTTCAT 38
 RESULT 39
 AAX27242
 ID AAX27242 standard; DNA; 40 BP.
 XX
 AC AAX27242;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE PCR primer for Tetanus toxin fragment C coding sequence.
 XX
 KW Tetanus toxin fragment C; TTC; central nervous system; CNS; spinal cord;

KW proteolytic fragment; retrograde axonal transport; spinal cord disease;
 KW transynaptic transport; neurodegenerative disease; motoneuron disease;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; therapy; ALS;
 KW SMA; neurodegenerative lysosomal storage disease; neuronal mapping;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Clostridium tetani.
 XX
 PN WO9909057-A2.
 XX
 PD 25-FEB-1999.
 XX
 PF 12-AUG-1998; 98WO-EP05113.
 XX
 PR 13-NOV-1997; 97US-0065236.
 PR 14-AUG-1997; 97US-0055615.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Brulet P, Coen L, Osta Pinzolas R;
 XX
 DR WPI; 1999-180971/15.
 XX
 PT Delivery of a composition to the central nervous system or spinal
 PT cord - comprises administration of a non-toxic, proteolytic
 PT fragment of tetanus toxin in association with a molecule having
 PT biological function
 XX
 PS Example 1; Page 19; 53pp; English.
 XX
 CC This sequence represents a PCR primer for DNA encoding the tetanus toxin
 CC fragment C (TTC). The invention relates to a method for in vivo delivery
 CC of a desired composition into a human or animal central nervous system
 CC (CNS) or spinal cord comprising administering a non-toxic, proteolytic
 CC fragment of tetanus toxin (TT) in association with at least a molecule
 CC having a biological function and where the composition is capable of in
 CC vivo retrograde axonal transport and transynaptic transport into the CNS
 CC or the spinal cord of the human or animal and of being delivered to
 CC different areas of the CNS or the spinal cord. The method can be used for
 CC the treatment of humans or animals with CNS or spinal cord disease,
 CC e.g. neurodegenerative and motoneuron diseases such as amyotrophic
 CC lateral sclerosis (ALS), spinal muscular atrophies (SMA) or
 CC neurodegenerative lysosomal storage diseases. Compositions comprising
 CC hybrid fragments of TT comprising fragments C and B can also be used for
 CC neuronal mapping and immunisations. Use of TT comprising fragments A, B
 CC and C results in better transport of the fragment inside the organism
 CC compared with fragment C.
 XX
 SQ Sequence 40 BP; 9 A; 11 C; 10 G; 10 T; 0 other;
 Query Match 1.0%; Score 18.2; DB 20; Length 40;
 Best Local Similarity 74.2%; Pred. No. 3.9e+05;
 Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1376 GCAGTCTGTTTATAGACACATCTTTTGA 1406
 Db | | | | | | | | | | | | | | | | | | | |
 2 GCAGTCTGAGTCTAGACCACTGCTTTTGA 32
 RESULT 40
 AAL46329/c
 ID AAL46329 standard; DNA; 28 BP.
 XX
 AC AAL46329;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE M30 protein vector PCR primer SEQ ID NO: 23.
 XX
 KW Neurodegenerative disease; M30; M31; M32; M33; stroke;
 KW fragile X syndrome; Huntington's disease; Parkinson's disease;
 KW Alzheimer's disease; multiple sclerosis; ovarian cancer;

KW neurodegeneration; immune disorder; autoimmune disease; allergy;
 KW infection; leukaemia; inflammation; neuroprotective; cerebroprotective;
 KW immunosuppressive; cytostatic; nootropic; antiparkinsonian; anti-allergic;
 KW virucide; anti-inflammatory; PCR; primer; ss.
 XX Unidentified.
 OS
 XX WO20021138-A2.
 PN
 XX
 XX 14-MAR-2002.
 PD
 XX
 XX
 XX 07-SEP-2001; 2001WO-EP10366.
 PF
 XX
 XX 07-SEP-2000; 2000US-0657479.
 PR
 XX
 XX (AXAR-) AXARON BIOSCIENCE AG.
 PA
 XX
 XX Schneider A, Hiemisch H, Rossner M, Klugmann M, Naim J;
 PI Eisenhardt G, Kuner R, Lanahan A, Worley P, Spielvogel D;
 PI Scheek S;
 XX
 XX WPI; 2002-292287/33.
 DR
 XX
 XX Diagnosis of neurodegenerative disease comprises detecting level of
 PT M30-family proteins -
 PT
 XX
 XX Example 14; Page 121; 130pp; German.
 PS
 XX
 XX The present invention relates to a method of diagnosing neurodegenerative
 CC diseases, comprising determining the concentration of a protein in a body
 CC sample, where the protein may be M30 or a variant thereof, M31, M32 or
 CC M33. The method is used to diagnose neurodegenerative diseases,
 CC particularly stroke but also e.g. fragile X syndrome, Huntington's,
 CC Parkinson's and Alzheimer's diseases, multiple sclerosis etc. Also
 CC overexpression of M31 can be used for diagnosis of carcinoma and sarcoma,
 CC especially ovarian cancer. The proteins can be used to identify specific
 CC ligands, potentially useful for treating neurodegeneration, immune-system
 CC disorders (e.g. autoimmune diseases, allergy, viral infection,
 CC leukaemia, inflammation etc.), carcinoma and sarcoma. Inhibitors of the
 CC interaction between the proteins and the protein kinase IRAK-1 can be
 CC used to treat neurodegeneration. The present sequence is a PCR primer for
 CC a coding sequence of a protein used in the method of the invention.
 XX
 SQ Sequence 28 BP; 8 A; 7 C; 7 G; 6 T; 0 other;
 Query Match 1.0%; Score 18; DB 24; Length 28;
 Best Local Similarity 80.8%; Pred. No. 3.7e+05;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 723 TCTTCATGCTGTGCATGAATGACC 748
 Db 26 TCTTCATGCTGGGAGAGATTCGATC 1
 RESULT 41
 ID AAI68954/c
 ID AAI68954 standard; DNA; 32 BP.
 XX
 AC AAI68954;
 AC
 XX 29-JAN-2002 (first entry)
 DT
 XX
 XX Activated T-cell derived DNA fragment, #90.
 DE
 XX
 XX Activated T-cell; immunosuppressive; immunostimulant; anti-inflammatory;
 KW cytostatic; gene therapy; vaccine; allergen; transplant rejection;
 KW guest versus host disease; malignant disease; ds.
 XX
 XX Homo sapiens.
 OS
 XX DE10021834-A1.
 PN
 XX 15-NOV-2001.
 XX

XX 06-MAY-2000; 2000DE-1021834.
 PF
 XX 06-MAY-2000; 2000DE-1021834.
 PR
 XX (LYNX-) LYNX THERAPEUTICS GMBH.
 PA
 XX
 XX Kramer MD, Winter H, Reinartz J;
 PI
 XX WPI; 2002-027320/04.
 DR
 XX
 XX New mRNA indicative of T cell activation and functional status, useful
 PT for diagnosis and therapy e.g. of autoimmunity or transplant rejection
 PT
 XX
 XX Claim 1; Page 30; 94pp; German.
 PS
 XX
 XX This sequence represents a novel messenger RNA, (mRNA), (I), for use as
 CC indicator of the activation and functional status of T cells, that have
 CC increased or reduced expression, and are present at higher or lower
 CC concentration, in activated T cells, relative to normal or resting cells,
 CC where (I) hybridizes to any of 334 sequences, reproduced, or their
 CC derivatives, complements or fragments. The products of the invention
 CC have immunosuppressive, immunostimulant, anti-inflammatory and cytostatic
 CC activity and can be used for gene therapy. The polynucleotides of the
 CC invention are used: (i) as reagent for detecting activation/functional
 CC status of T cells, for diagnosis, therapy, modulation or control of the
 CC status, in cases of (auto)immunity (against microorganisms, vaccines or
 CC allergens); transplant rejection; immunologically-related inflammation;
 CC immunosuppression; immune deficiency; guest versus host disease, and
 CC malignant diseases of the immune system; (ii) for identifying agents,
 CC potential pharmaceuticals, that bind to (II) or derived polypeptides
 CC (III); (iii) to prepare kits for measuring gene expression profiles in
 CC isolated immune, especially T, cells; (iv) to raise antibodies (Ab)
 CC directed against (III); and (v) to prepare binding molecules (IV)
 CC specific for (III). Ab and (iv) are also useful for detecting and
 CC modulating the activation and functional status of T cells.
 CC AAI68865-AAI69198 represent the activated T-cell derived polynucleotide
 CC fragments described in the method of the invention.
 XX
 SQ Sequence 32 BP; 14 A; 6 C; 6 G; 6 T; 0 other;
 Query Match 1.0%; Score 18; DB 24; Length 32;
 Best Local Similarity 80.8%; Pred. No. 4e+05;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1592 GCTCAACTCTATCATGTTTGTGTAAT 1617
 Db 27 GCTAGCAGTCTATCAATTTTGTGTAT 2
 RESULT 42
 ID ABV72966
 ID ABV72966 standard; DNA; 33 BP.
 XX
 AC ABV72966;
 AC
 XX 08-JAN-2003 (first entry)
 DT
 XX
 XX Human FWMP protein 60 cDNA cloning PCR primer 3.
 DE
 XX
 XX FWMP protein 60; tumour; nosohemia; HIV infection; immunological disease;
 KW inflammation; human; PCR; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX CN1307055-A.
 PN
 XX
 XX 08-AUG-2001.
 PD
 XX
 XX 28-JAN-2000; 2000CN-0111613.
 PF
 XX 28-JAN-2000; 2000CN-0111613.
 XX

XX PA (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
 XX PI Mao Y, Xie Y;
 XX DR WPI; 2002-049884/07.
 XX XX New polypeptide, useful for treating diseases, comprises the human PWMP
 PT protein 60 and polynucleotide for coding said polypeptide -
 XX XX Example 5; Page 17 (disclosure); 34pp; Chinese.
 XX XX The invention relates to a novel human PWMP protein 60 polypeptide, and
 CC encoding polynucleotides. The polypeptide can be expressed by standard
 CC DNA recombination. The PWMP protein 60 polypeptide, polynucleotide and
 CC modulators are useful for treating various diseases, such as malignant
 CC tumour, nosohemia, HIV infection, immunological diseases and
 CC inflammations. The present sequence represents the human PWMP protein 60
 CC cDNA cloning PCR primer.
 XX XX Sequence 33 BP; 12 A; 8 C; 3 G; 10 T; 0 other;
 SQ
 Query Match 1.0%; Score 18; DB 24; Length 33;
 Best Local Similarity 80.8%; Pred. No. 4e+05;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1455 TGGGGTATTTCATTAACAATACTTTG 1480
 DB 8 TGATGTCATCAATAACAATACTTTG 33
 RESULT 43
 AAS44188/c
 ID AAS44188 standard; DNA; 34 BP.
 XX AC AAS44188;
 XX DT 18-DEC-2001 (first entry)
 XX DE Neisseria meningitidis B MC58 genomic DNA sequence PCR primer #283.
 XX KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1; ss;
 XX KW Neisserial protein; PCR primer.
 XX OS Neisseria meningitidis.
 XX OS Synthetic.
 XX PN WO200164922-A2.
 XX PD 07-SEP-2001.
 XX PF 28-FEB-2001; 2001WO-IB00452.
 XX PR 28-FEB-2000; 2000GB-0004695.
 XX PR 13-NOV-2000; 2000GB-0027675.
 XX PA (CHIR-) CHIRON SPA.
 XX PI Arico MB, Comanducci M, Galeotti C, Massignani V, Guiliani MM;
 PI Pizza M;
 XX WPI; 2001-582163/65.
 XX PT Producing heterologous proteins from Neisseria meningitidis and N.
 PT gonorrhoeae -
 XX XX Disclosure; Page 87; 119pp; English.
 XX XX The invention relates to methods for the heterologous expression of
 CC Neisserial proteins from Neisseria meningitidis and Neisseria
 CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
 CC leader peptide, and may be replaced by a domain from a different protein
 CC to make a fusion protein, in order to enhance heterologous expression of

CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
 CC stretch, can be mutated to enhance expression. The proteins used in the
 CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
 CC AAS43807-AAS43867 and AAS43906-AAS44358 represent PCR primers used in the
 CC methods of the invention.
 XX XX Sequence 34 BP; 13 A; 9 C; 8 G; 4 T; 0 other;
 SQ
 Query Match 1.0%; Score 18; DB 22; Length 34;
 Best Local Similarity 70.6%; Pred. No. 4.1e+05;
 Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 443 CTCGCTGGGATGTTCTTGTATGGGATGCGC 476
 DB 34 CTTTCTGGGATGTTCTTGTATGGGATGCGC 1
 RESULT 44
 ABX05700
 ID ABX05700 standard; DNA; 36 BP.
 XX AC ABX05700;
 XX DT 11-FEB-2003 (first entry)
 XX DE PCR primer for knock out of S. pneumoniae gene SEQ ID 3480 #4.
 XX KW PCR; ss; bacterial meningitis; pneumonia; sepsis; otitis media;
 KW ear infection; antiinflammatory; antibacterial; immunostimulant;
 KW auditory; respiratory; gene therapy; vaccine; primer.
 XX OS Streptococcus pneumoniae type 4 strain.
 XX PN WO200277021-A2.
 XX PD 03-OCT-2002.
 XX PF 27-MAR-2002; 2002WO-IB02163.
 XX PR 27-MAR-2001; 2001GB-0007658.
 XX PA (CHIR-) CHIRON SPA.
 XX PA (GENO-) INST GENOMIC RES.
 XX PI Massignani V, Tettelin H, Fraser C;
 XX WPI; 2003-040579/03.
 XX XX New proteins and nucleic acid molecules from Streptococcus pneumoniae,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media
 PT or ear infection -
 XX XX Disclosure; Page 42; 56pp; English.
 XX XX The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as
 CC ABS56454. Also included are an antibody which binds one of the
 CC proteins, treating a patient by administering the protein, DNA or
 CC antibody (in a composition), a kit comprising first and second primers,
 CC which are the nucleic acid cited above or fragments between nucleotides
 CC 8-100 of a sequence not defined in the specification, for amplifying a
 CC target sequence contained within a Streptococcus nucleic acid sequence,
 CC where the first primer is substantially complementary to the target
 CC sequence and the second primer is substantially complementary to the
 CC complement of the target sequence, and where the parts of the primers
 CC having substantial complementarity define the termini of the target
 CC sequence to be amplified, assay comprising contacting a test compound
 CC with the protein, and determining whether the test compound binds to the
 CC protein and a Streptococcus pneumoniae bacterium, where one or more

CC genes encoding the proteins has been rendered inactive. The proteins,
CC nucleic acid molecules, antibody and compositions are useful as
CC medicaments for treating or preventing a disease or infection due to
CC streptococcus bacteria, particularly *S. pneumoniae*, such as pneumonia,
CC sepsis, otitis media or ear infection. They are also useful in developing
CC vaccines, diagnostics and antibiotics. The methods are useful for
CC identifying immunodominant proteins. The present sequence is a PCR
CC primer used in a knock-out experiment for one of the 2489 identified
CC coding region from the genomic sequence.

XX Sequence 36 BP; 3 A; 8 C; 7 G; 18 T; 0 other;

Query Match 1.0%; Score 18; DB 25; Length 36;

Best Local Similarity 70.6%; Pred. No. 4.2e+05;

Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 360 TCCTTCGGGAGCTGTCTTCTGAACTCTTTTGCT 393

DB 3 TAGCGGCGCAATGTCTTCTGCTCTTTTGCT 36

RESULT 45

ABK58002/c

ID ABK58002 standard; RNA; 38 BP.

XX AC ABK58002;

DT 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #2373.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease, COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.

XX Homo sapiens.

XX WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US24970.

XX 09-AUG-2000; 2000US-224383P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

PI Thompson J, McSwiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma -

XX Claim 5; Page 56; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the

CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention.

XX Sequence 38 BP; 8 A; 8 C; 10 G; 12 U; 0 other;

Query Match 1.0%; Score 18; DB 24; Length 38;

Best Local Similarity 70.6%; Pred. No. 4.3e+05;

Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1808 GGACTTTAGTCCAAAGGCCCTGTGTATTAAA 1841

DB 35 GGACTTTCGGCCTAACGGCCTCATCATGATGAAA 2

Search completed: October 23, 2003, 09:41:44

Job time : 500 secs

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Perfect score: 1864
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 1792395 seqs, 1340900451 residues
Total number of hits satisfying chosen parameters: 1060730
Minimum DB seq length: 10
Maximum DB seq length: 40
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications, NA:*

1: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	1.1	40	10	US-09-780-929-53
2	19	1.0	35	9	US-09-152-059-56
3	19	1.0	35	12	US-10-008-029-56
4	19	1.0	35	12	US-10-208-650-56
5	18.8	1.0	31	10	US-09-825-124B-12
6	18.8	1.0	39	10	US-09-974-973-7
7	18.6	1.0	25	14	US-10-098-263B-33220
8	18.2	1.0	33	12	US-09-882-945A-151
9	18.2	1.0	39	14	US-10-193-412A-9
10	18.2	1.0	40	11	US-09-816-467-13
11	17.8	1.0	31	9	US-09-801-274-1689
12	17.8	1.0	35	12	US-10-292-896-25
13	17.8	1.0	38	11	US-09-877-478-2673
14	17.8	1.0	38	11	US-09-776-474-2153
15	17.8	1.0	39	9	US-09-732-914-119
16	17.8	1.0	39	10	US-09-922-261-132

17	17.8	1.0	40	11	US-09-738-444A-1	Sequence 1, Appli
18	17.6	0.9	33	10	US-09-805-761-28	Sequence 28, Appl
19	17.4	0.9	25	12	US-10-083-246A-162	Sequence 162, App
20	17.4	0.9	35	9	US-09-861-696-46	Sequence 46, Appl
21	17.4	0.9	35	10	US-09-464-099A-46	Sequence 46, Appl
22	17.4	0.9	40	12	US-10-157-391-89	Sequence 89, Appl
23	17.4	0.9	40	12	US-10-157-391-89	Sequence 89, Appl
24	17.4	0.9	40	12	US-10-157-096-89	Sequence 89, Appl
25	17.4	0.9	40	12	US-10-157-215A-89	Sequence 89, Appl
26	17.4	0.9	40	12	US-10-157-302-89	Sequence 89, Appl
27	17.4	0.9	40	12	US-10-154-951B-89	Sequence 89, Appl
28	17.4	0.9	40	12	US-10-157-239-89	Sequence 89, Appl
29	17.4	0.9	40	14	US-10-184-007A-2	Sequence 2, Appli
30	17.2	0.9	25	14	US-10-098-263B-21714	Sequence 21714, A
31	17.2	0.9	32	12	US-10-276-372-24	Sequence 24, Appl
32	17.2	0.9	32	12	US-10-335-394-36	Sequence 26, Appl
33	17.2	0.9	33	9	US-09-812-133-3	Sequence 3, Appli
34	17.2	0.9	35	13	US-10-109-886-2	Sequence 2, Appli
35	17.2	0.9	37	13	US-10-027-632-75809	Sequence 75809, A
36	17.2	0.9	38	10	US-09-960-428-1	Sequence 1, Appli
37	17.2	0.9	38	11	US-09-730-289B-2369	Sequence 2369, Ap
38	17.2	0.9	38	11	US-09-776-474-1355	Sequence 1355, Ap
39	17.2	0.9	38	13	US-10-045-815-13	Sequence 13, Appl
40	17.2	0.9	39	12	US-10-186-185-10	Sequence 10, Appl
41	17.2	0.9	40	11	US-09-998-425-45	Sequence 45, Appl
42	17.2	0.9	40	11	US-09-997-977-45	Sequence 45, Appl
43	17	0.9	25	14	US-10-098-263B-33219	Sequence 33219, A
44	17	0.9	25	14	US-10-098-263B-45507	Sequence 45507, A
45	17	0.9	25	14	US-10-098-263B-59260	Sequence 59260, A

ALIGNMENTS

RESULT 1

US-09-780-929-53
; Sequence 53, Application US/09780929
; Patent No. US20020151693A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Breaker, Ronald
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-H (500/001)
; CURRENT APPLICATION NUMBER: US/09780,929
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: US 60/181,360
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 40
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-929-53

Query Match 1.1%; Score 20.4; DB 10; Length 40;
Best Local Similarity 47.4%; Pred. No. 1.1e+05;
Matches 18; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 883 GAATTCGGTTTGGGAATGGATTTTAAAGGAGGGTATG 920

Db 3 GCAUUGCGUUGAGAACUGGAAGUUGAAGAGGGCAUG 40

RESULT 2

US-09-152-059-56/C
; Sequence 56, Application US/09152059
; Patent No. US20020068708A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER

; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/09/152,059
; CURRENT FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-152-059-56

Query Match 1.0%; Score 19; DB 9; Length 35;
Best Local Similarity 71.4%; Pred. No. 2.4e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1582 AATGACAACAGCTACAACTCTATCAGTTTGTGTTAA 1616
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35 AAGTACAACAGCGACAAGTCCAGCACCTACGTTAA 1

RESULT 3
US-10-008-029-56/c
; Sequence 56, Application US/10008029
; Publication No. US20030134808A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-56

Query Match 1.0%; Score 19; DB 12; Length 35;
Best Local Similarity 71.4%; Pred. No. 2.4e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1582 AATGACAACAGCTACAACTCTATCAGTTTGTGTTAA 1616
||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35 AAGTACAACAGCGACAAGTCCAGCACCTACGTTAA 1

RESULT 4
US-10-208-650-56/c
; Sequence 56, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-56

Query Match 1.0%; Score 19; DB 12; Length 35;
Best Local Similarity 71.4%; Pred. No. 2.4e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1582 AATGACAACAGCTACAACTCTATCAGTTTGTGTTAA 1615
||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35 AAGTACAACAGCGACAAGTCCAGCACCTACGTTAA 1

RESULT 5
US-09-825-124B-12
; Sequence 12, Application US/09825124B
; Patent No. US20020151072A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Ramesh
; APPLICANT: Metz, Richard
; TITLE OF INVENTION: Improved Chimeric Mutational Vectors
; FILE REFERENCE: 7991-091-999
; CURRENT APPLICATION NUMBER: US/09/825,124B
; CURRENT FILING DATE: 2001-04-03


```

; Sequence 13, Application US/09816467
; Publication No. US20030004121A1
; GENERAL INFORMATION:
; APPLICANT: COEN, LAURENT
; APPLICANT: PINZOLAS, ROSARIO OSTA
; APPLICANT: BRULET, PHILIPPE
; TITLE OF INVENTION: HYBRID PROTEINS THAT MIGRATE RETROGRADELY AND
; FILE REFERENCE: 03495.0174-01000
; CURRENT APPLICATION NUMBER: US/09/816,467
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/055,615
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: 60/065,236
; PRIOR FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-816-467-13

```

```

Query Match 1.0%; Score 18.2; DB 11; Length 40;
Best Local Similarity 74.2%; Pred. No. 4.3e+05;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1376 GCAGTCTGTTTATAGCACATTTCTTTTGA 1406
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 GCAGTCTCGAGTCTAGACCATGCTTTTGA 32

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RESULT 11
US-09-801-274-1689/c
; Sequence 1689, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1689
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1689

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Query Match 1.0%; Score 17.8; DB 9; Length 31;
Best Local Similarity 75.9%; Pred. No. 4.7e+05;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1400 TTTTGAAGAAATTCATAGATTGCA 1428
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 TTTTGAAGACAATCAGGTTTATGCA 1

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RESULT 12
US-10-292-896-25/c
; Sequence 25, Application US/10292896
; Publication No. US20030186850A1
; GENERAL INFORMATION:
; APPLICANT: HASSAN, Helle

```

```

; APPLICANT: REIS, Celso A.
; APPLICANT: BENNETT, Eric P.
; APPLICANT: CLAUSEN, Henrik
; TITLE OF INVENTION: METHODS TO IDENTIFY AGENTS MODULATING FUNCTIONS OF POLYPEPTIDE GAI
; TITLE OF INVENTION: TRANSFERASES, PHARMACEUTICAL COMPOSITIONS COMPRISING SUCH AGENTS
; FILE REFERENCE: 4305/1H154-US3
; CURRENT APPLICATION NUMBER: US/10/292,896
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/425,204
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/DK01/00328
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 60/203,331
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer EBHC75D
US-10-292-896-25

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```

Query Match 1.0%; Score 17.8; DB 12; Length 35;
Best Local Similarity 75.9%; Pred. No. 5.1e+05;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 998 GAAGCTGGTCTTCTCTAGAGACTTCG 1026
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 GATGAAGGCTCTTCTTTTAAAGATTCCG 2

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RESULT 13
US-09-877-478-2673/c
; Sequence 2673, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2673
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-2673

```

```

RESULT 17
US-09-738-444A-1
; Sequence 1, Application US/0973844A
; Publication No. US2003002317A1
; GENERAL INFORMATION:
; APPLICANT: Jack, William E.
; APPLICANT: Schildkraut, Ira
; APPLICANT: Menin, Julie F.
; APPLICANT: Greenough, Lucia
; TITLE OF INVENTION: Use of Site-Specific Nicking Endonucleases to Create
; TITLE OF INVENTION: Single-Stranded Regions And Applications Thereof
; FILE REFERENCE: NEB-180
; CURRENT APPLICATION NUMBER: US/09/738,444A
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-738-444A-1
Query Match 1.0% Score 17.8 DB 11 Length 40:

```

Best Local Similarity 75.9%; Pred. No. 5.5e+05;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1753 AAATAAGTACCGTAAACTTAATCTAAC 1781
|||||
Db 11 AAAGTATATACCGTAAACTTGTCTGAC 39

RESULT 18
US-09-805-761-28/c
; Sequence 28, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; TITLE OF INVENTION: VEGF OLIGONUCLEOTIDES
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VEGF antisense oligonucleotide
US-09-805-761-28

Query Match 0.9%; Score 17.6; DB 10; Length 33;
Best Local Similarity 71.9%; Pred. No. 5.6e+05;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1498 TCGTGAAGATCGCCAAAGCGAAGCTGTTTACC 1529
|||||
Db 32 TCGAGTACATCTTCAAGCCATCTGTGTGCC 1

RESULT 19
US-10-083-246A-162
; Sequence 162, Application US/10083246A
; Publication No. US20030152936A1
; GENERAL INFORMATION:
; APPLICANT: Athena Diagnostics
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNEY
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 1133/2002
; CURRENT APPLICATION NUMBER: US/10/083,246A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: Synthetic primer
US-10-083-246A-162

Query Match 0.9%; Score 17.4; DB 12; Length 25;

Best Local Similarity 94.7%; Pred. No. 5.3e+05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 711 TGACTAAATTTTCTTCAT 729
|||||
Db 7 TGACTAAATTTTCTTCTT 25

RESULT 20
US-09-861-696-46
; Sequence 46, Application US/09861696
; Patent No. US20020007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENO1PYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861,696
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-861-696-46

Query Match 0.9%; Score 17.4; DB 9; Length 35;
Best Local Similarity 77.8%; Pred. No. 6.5e+05;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1026 GTATTCAACATTTGATCTTCAGAA 1052
|||||
Db 2 GAAATCAAACTTCAGATCTTGAGATA 28

RESULT 21
US-09-464-099A-46
; Sequence 46, Application US/09464099A
; Patent No. US2002016860A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENO1PYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31

; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-215A-89

Query Match 0.9%; Score 17.4; DB 12; Length 40;
Best Local Similarity 68.6%; Pred. No. 7.1e+05;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 301 CTGTGGCTTGGCAATGCTTATTGTTTGTATGACG 335
DB 5 CGGTACCTTATCAATGGTGTATGATGACG 39

RESULT 26
US-10-157-302-89
; Sequence 89, Application US/10157302
; Publication No. US20030190683A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED RATIONAL DRUG DESIGN
; FILE REFERENCE: MPEX.008DV17
; CURRENT APPLICATION NUMBER: US/10/157,302
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-302-89

Query Match 0.9%; Score 17.4; DB 12; Length 40;
Best Local Similarity 68.6%; Pred. No. 7.1e+05;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 301 CTGTGGCTTGGCAATGCTTATTGTTTGTATGACG 335
DB 5 CGGTACCTTATCAATGGTGTATGATGACG 39

RESULT 27
US-10-154-951B-89
; Sequence 89, Application US/10154951B
; Publication No. US20030194798A1
; GENERAL INFORMATION:
; APPLICANT: Surber, Mark W.
; APPLICANT: Sabbadini, Roger A.
; TITLE OF INVENTION: MINICELL COMPOSITIONS AND METHODS
; FILE REFERENCE: MPEX.008A
; CURRENT APPLICATION NUMBER: US/10/154,951B
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843

; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer.
US-10-154-951B-89

Query Match 0.9%; Score 17.4; DB 12; Length 40;
Best Local Similarity 68.6%; Pred. No. 7.1e+05;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 301 CTGTGGCTTGGCAATGCTTATTGTTTGTATGACG 335
DB 5 CGGTACCTTATCAATGGTGTATGATGACG 39

RESULT 28
US-10-157-299-89
; Sequence 89, Application US/10157299
; Publication No. US20030194714A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED TRANSFORMATION
; FILE REFERENCE: MPEX.008DV15
; CURRENT APPLICATION NUMBER: US/10/157,299
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-299-89

Query Match 0.9%; Score 17.4; DB 12; Length 40;
Best Local Similarity 68.6%; Pred. No. 7.1e+05;
Matches 24; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 301 CTGTGGCTTGGCAATGCTTATTGTTTGTATGACG 335
DB 5 CGGTACCTTATCAATGGTGTATGATGACG 39

RESULT 29
US-10-184-007A-2
; Sequence 2, Application US/10184007A
; Publication No. US20030091546A1
; GENERAL INFORMATION:
; APPLICANT: Chiron Corporation
; TITLE OF INVENTION: Methods of Suppressing Immune Response by Gene Therapy
; FILE REFERENCE: 20263.440
; CURRENT APPLICATION NUMBER: US/10/184,007A
; CURRENT FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: DNA
; ORGANISM: artificial

FEATURE:
OTHER INFORMATION: reverse primer
US-10-184-007A-2

Query Match 0.9%; Score 17.4; DB 14; Length 40;
Best Local Similarity 77.8%; Pred. No. 7.1e+05;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 665 ACATTCATTTTGGAGATTTCTCTTCA 691
DB 4 ATATCGATTCAAGGCATTTCTTTTCA 30

RESULT 30

US-10-098-263B-21714/c
Sequence 21714, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 21714
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-263B-21714

Query Match 0.9%; Score 17.2; DB 14; Length 25;
Best Local Similarity 86.4%; Pred. No. 6e+05;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1587 CAACAGCTACAACTCTATCAGT 1608
DB 25 CAACAGGTACATCTGTATCAGT 4

RESULT 31

US-10-276-372-24/c
Sequence 24, Application US/10276372
Publication No. US20030186269A1
GENERAL INFORMATION:
APPLICANT: Bahr, Georges
APPLICANT: Cocude, Cecile
APPLICANT: Capron, Andre
TITLE OF INVENTION: SSA-56 kDa Polypeptide and its Fragments and Polynucleotides
TITLE OF INVENTION: Encoding said Polypeptide and Therapeutic Uses
FILE REFERENCE: 017753-171
CURRENT APPLICATION NUMBER: US/10/276,372
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: FR 06/06315
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/FR 01/00725
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-10-276-372-24

Query Match 0.9%; Score 17.2; DB 12; Length 30;
Best Local Similarity 73.3%; Pred. No. 6.7e+05;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 565 CAAGGCTTTTGGAGCCATTTTTCATTCTAA 594
||||| | | | | | | | | | | |

DB 30 CAAGGCTGTGGGATCCATGCATGCTTCTCA 1

RESULT 32

US-10-335-394-26/c
Sequence 26, Application US/10335394
Publication No. US20030138452A1
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Bitagyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/10/335,394
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/09/646,028
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-26

Query Match 0.9%; Score 17.2; DB 12; Length 32;
Best Local Similarity 73.3%; Pred. No. 7e+05;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 450 GGATTGTTCTTGGGATGGCGGTAG 479
DB 30 GGACCGTCTTCGAGAGGGATGGCCATGG 1

RESULT 33

US-09-812-133-3
Sequence 3, Application US/09812133
Patent No. US20020065240A1
GENERAL INFORMATION:
APPLICANT: Thomas, Kenneth A., Jr.
APPLICANT: Kendall, Richard L.
APPLICANT: Bett, Andrew J.
APPLICANT: Huckle, William R.
TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: 20073P
CURRENT APPLICATION NUMBER: US/09/812,133
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: PCT/US98/22668
PRIOR FILING DATE: 1998-10-23
PRIOR APPLICATION NUMBER: 60/063,629
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
US-09-812-133-3

Query Match 0.9%; Score 17.2; DB 9; Length 33;
Best Local Similarity 73.3%; Pred. No. 7.1e+05;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1673 GGGATTCTTCTAGGAACATTATCGTCTCTT 1702
DB 3 GGGATCCAAATATGAACCTTTCTGCTCTCTT 32
||||| | | | | | | | | | | |

RESULT 34
 US-10-109-886-2
 ; Sequence 2, Application US/10109886
 ; Publication No. US20020119499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANABE SEIYAKU CO. LTD.
 ; APPLICANT: TANIGUCHI, Tomoyasu
 ; APPLICANT: MIZUKAMI, Junko
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND
 ; TITLE OF INVENTION: ANTAGONIST TO PPAR
 ; FILE REFERENCE: TANIGUCHI=6
 ; CURRENT APPLICATION NUMBER: US/10/109,886
 ; PRIOR FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 09/514,247
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: PCT/JP98/03734
 ; PRIOR FILING DATE: 1998-08-24
 ; PRIOR APPLICATION NUMBER: JP231084/1997
 ; PRIOR FILING DATE: 1997-08-27
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 35
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificially synthesized primer sequence
 US-10-027-632-75809-2
 Query Match 0.9%; Score 17.2; DB 13; Length 35;
 Best Local Similarity 73.3%; Pred. No. 7.4e+05; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 127 CCCATTGAAATCATGCCAGTGTCTCAGG 156
 Db 1 CCGCTCGAGAAATGTTGGCAGTGGCTCAGG 30
 RESULT 35
 US-10-027-632-75809
 ; Sequence 75809, Application US/10027632
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.129
 ; CURRENT APPLICATION NUMBER: US/10/027,632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 75809
 ; LENGTH: 37
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-75809
 Query Match 0.9%; Score 17.2; DB 13; Length 37;
 ; Sequence 1355, Application US/09776474

Best Local Similarity 64.7%; Pred. No. 7.6e+05;
 Matches 22; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 QY 66 TTTGACATTGATTTAGGAATTTCTCTTCAATG 694
 Db 2 TTTGATATTGCTCTTARHAAATTTSGATSTAATG 35
 RESULT 36
 US-09-960-428-1
 ; Sequence 1, Application US/09960428
 ; Patent No. US20020115147A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roche Diagnostics GmbH
 ; TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokaryotic
 ; FILE REFERENCE: 5272/00/
 ; CURRENT APPLICATION NUMBER: US/09/960,428
 ; CURRENT FILING DATE: 2001-09-21
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 38
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-09-960-428-1
 Query Match 0.9%; Score 17.2; DB 10; Length 38;
 Best Local Similarity 73.3%; Pred. No. 7.7e+05;
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1347 CTTTAAATCATGACCTTTTGGCTACTGTG 1376
 Db 6 CTGGAATTCATGACTGTTGCGCTACATCTG 35
 RESULT 37
 US-09-730-2898-2369/c
 ; Sequence 2369, Application US/09730289B
 ; Publication No. US20030050259A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
 ; FILE REFERENCE: MBH00-864-A (400/006)
 ; CURRENT APPLICATION NUMBER: US/09/730,289B
 ; CURRENT FILING DATE: 2000-12-05
 ; PRIOR APPLICATION NUMBER: US 60/169,100
 ; PRIOR FILING DATE: 1999-12-06
 ; NUMBER OF SEQ ID NOS: 3897
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2369
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-730-2898-2369
 Query Match 0.9%; Score 17.2; DB 11; Length 38;
 Best Local Similarity 65.8%; Pred. No. 7.7e+05;
 Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1226 AGCAAACTATCGAAGAAATGCGTTATCAGCGACCAT 1263
 Db 38 AGCCTACTTTCGCGCTAACGGCCTCATCAGTTGACCAT 1
 RESULT 38
 US-09-776-474-1355
 ; Sequence 1355, Application US/09776474

Publication No. US20030087847A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Jarvis, Thale
APPLICANT: Boher, Robert
APPLICANT: Holman, Patricia
APPLICANT: Fattaey, Ali

APPLICANT: McSwiggen, Jim

TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK

FILE REFERENCE: MBH00-955-A (400/008)

CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: US 60/179,983

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 2992

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1355

LENGTH: 38

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-776-474-1355

Query Match 0.9%; Score 17.2; DB 11; Length 38;

Best Local Similarity 52.6%; Pred. No. 7.7e+05;

Matches 20; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1710 CACCACTCTGTTGTTTATGTCCTCGTAAGAAAT 1747

Db 1 CACCACCUUGAUGAGCGGUAGGCGGAAGAGUGACU 38

RESULT 39

US-10-045-815-13

Sequence 13, Application US/10045815

Publication No. US20020160498A1

GENERAL INFORMATION:

APPLICANT: Wadhwa, Renu

APPLICANT: Sugihara, Takashi

APPLICANT: Ohide, Akiko

TITLE OF INVENTION: TUMOR SUPPRESSOR GENE

FILE REFERENCE: 06501-091001

CURRENT APPLICATION NUMBER: US/10/045,815

PRIOR FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/JP00/02731

PRIOR FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: JP 11/118806

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13

LENGTH: 38

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificially Synthesized Primer Sequence

US-10-045-815-13

Query Match 0.9%; Score 17.2; DB 13; Length 38;

Best Local Similarity 73.3%; Pred. No. 7.7e+05;

Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1289 ATCTGCTCTATGTAGTTGGCTTTGAA 1318

Db 3 ATCTAGATCTATGGCGGTACGCGGTGAA 32

RESULT 40

US-10-186-185-10/c

Sequence 10, Application US/10186185

Publication No. US20030138412A1

GENERAL INFORMATION:

APPLICANT: GOODRICH, DAVID W.

APPLICANT: YIN, SHENMIN

APPLICANT: DOOSTZADEH-CIZERON, JALEH

TITLE OF INVENTION: INHIBITION OF TUMOR GROWTH AND METASTASIS BY N5 GENE

FILE REFERENCE: UTSC:700US

CURRENT APPLICATION NUMBER: US/10/186,185

CURRENT FILING DATE: 2002-06-27

PRIOR APPLICATION NUMBER: 60/301,619

PRIOR FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 39

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Primer

US-10-186-185-10

Query Match 0.9%; Score 17.2; DB 12; Length 39;

Best Local Similarity 65.8%; Pred. No. 7.9e+05;

Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 744 AGACCCACATACACAGTTGCATATGATGAATAAGTTC 781

Db 38 ATACCAACCTACGAGATAATATGACGAGAGAGTTC 1

RESULT 41

US-09-998-425-45/c

Sequence 45, Application US/09998425

Publication No. US20030008346A1

GENERAL INFORMATION:

APPLICANT: Bartel, Paul L.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: MMS1 - An MMS1 Interacting Protein

FILE REFERENCE: MMS1 Gene

CURRENT APPLICATION NUMBER: US/09/998,425

CURRENT FILING DATE: 2001-12-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/233,086

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/071,861

PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-20

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 45

LENGTH: 40

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: MMS1 Primers

US-09-998-425-45

Query Match 0.9%; Score 17.2; DB 11; Length 40;

Best Local Similarity 65.8%; Pred. No. 8e+05; 13; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1603 ATCAGTTTGTAAATGCTTTTGTATAGCGGCTCCT 1640

Db 38 ATCAGTATTGTTGGTGGACATGGTCATAGCTGTTCT 1

RESULT 42

US-09-997-977-45/c

Sequence 45, Application US/09997977

Publication No. US20030027228A1

GENERAL INFORMATION:

APPLICANT: Bartel, Paul L.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Myriad Genetics, Inc.

```
; TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC1 Gene
; CURRENT APPLICATION NUMBER: US/09/997,977
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 09/233,086
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: US 60/071,861
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MMSC1 Primers
US-09-997-977-45
```

```
Query Match          0.9%; Score 17.2; DB 11; Length 40;
Best Local Similarity 65.8%; Pred. No. 8e+05;
Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1603 ATCAGTTTGTGTAATGCTTTTGTATAGCGGCTCCT 1640
||||| ||||| ||||| ||||| ||||| |||||
Db 38 ATCAGTATTGTTGGTGGACATGCTCATAGCTGTTCT 1
```

```
RESULT 43
US-10-098-263B-33219/c
; Sequence 33219, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 33219
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-33219
```

```
Query Match          0.9%; Score 17; DB 14; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.8e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1682 CTAGGAACATTTATCGTCTCTTTATA 1706
||||| ||||| ||||| ||||| |||||
Db 25 CTAGGATCATTAACGGATCTTTATA 1
```

```
RESULT 44
US-10-098-263B-45507
; Sequence 45507, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 45507
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: Homo sapien
US-10-098-263B-45507
```

```
Query Match          0.9%; Score 17; DB 14; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.8e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 909 AAGGAGGTATGCCCTTACCTTTAA 933
||||| ||||| ||||| ||||| |||||
Db 1 ACGGAGGTATTCTGTTTACCTGTAA 25
```

```
RESULT 45
US-10-098-263B-59260/c
; Sequence 59260, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59260
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-59260
```

```
Query Match          0.9%; Score 17; DB 14; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.8e+05;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 199 AAAATCTGAGCGCATGCTCTTTGTT 223
||||| ||||| ||||| ||||| |||||
Db 25 ACACCTCTGCAGAGTTGCTTTGTT 1
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Search completed: October 23, 2003, 12:45:20
Job time : 508 secs
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 02:21:56 ; Search time 500 Seconds
(without alignments)
10063.505 Million cell updates/sec

Title: US-09-868-987-1
Perfect score: 1864
Sequence: 1 atggacttcgcgcatattgtc.....atgacaaattcagataatgc 1864

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 2722572

Minimum DB seq length: 5
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
C 1	25.4	1.4	88	25	ABX55459 Bovine EST associa
C 2	25.2	1.4	96	22	AAK68003 Human immune/haema
C 3	25	1.3	94	25	ABZ78586 Tumour suppression
C 4	25	1.3	90	25	ABZ09133 Human oligonucleot
C 5	24.4	1.3	90	24	ABA82853 Human protective D
C 6	24.4	1.3	95	20	AAH07251 Genetic suppressor
C 7	24.4	1.3	95	22	AAF93098 Human HIV/tumorige
C 8	24.4	1.3	95	22	AAF94529 Genetic suppressor

9	24.4	1.3	95	24	ABT03434 Human HIV-inhibiti
10	24.2	1.3	65	24	ABN57082 Mouse spliced tran
C 11	24.2	1.3	97	16	AAT26550 Human gene signatu
C 12	24.2	1.3	97	22	AAK68002 Human immune/haema
C 13	24	1.3	64	24	AAD30164 c-myc-tagged mouse
C 14	24	1.3	65	24	ABZ23420 Candida gene relat
15	24	1.3	78	17	AAT38856 E. coli enterotoxi
16	24	1.3	78	22	AAH28270 Nucleotide sequenc
C 17	23.8	1.3	62	22	AAH09129 Anti-FLK-1 ribozym
C 18	23.8	1.3	62	22	AAH09130 Anti-FLK-1 ribozym
C 19	23.8	1.3	87	24	ABK76695 Bacillus lichenifo
C 20	23.8	1.3	89	22	AAH41939 Genomic sequence #
21	23.8	1.3	89	22	AAH41952 Genomic sequence #
C 22	23.6	1.3	60	24	ABN34358 Human spliced tran
C 23	23.6	1.3	65	24	ABZ28946 Candida gene relat
24	23.6	1.3	79	21	AAC11402 Human secreted pro
25	23.6	1.3	90	22	AAH23666 Tetracycline promo
C 26	23.6	1.3	98	24	ABK17244 Coupled ligation a
27	23.6	1.3	98	24	ABK17305 Coupled ligation a
C 28	23.6	1.3	99	21	AAH64962 Protein scaffold m
C 29	23.6	1.3	99	22	AAD16979 Oligonucleotide HF
C 30	23.6	1.3	99	24	ABN87086 Human 10 Fn3 gene
C 31	23.4	1.3	60	24	ABN32824 Human spliced tran
C 32	23.4	1.3	78	21	AAH53034 Arabidopsis thalia
C 33	23.4	1.3	84	22	AAK69024 Human immune/haema
C 34	23.4	1.3	87	16	AAT21076 Human gene signatu
C 35	23.4	1.3	94	21	AAC14189 Human secreted pro
36	23.2	1.2	60	24	ABN46009 Human spliced tran
C 37	23.2	1.2	60	24	ABN49485 Human spliced tran
38	23.2	1.2	70	21	AAH98467 Nucleotide sequenc
C 39	23.2	1.2	75	21	AAC15734 Human secreted pro
40	23.2	1.2	96	18	AAT65280 Platelet derived g
41	23.2	1.2	96	20	AAH87067 Platelet derived g
C 42	23	1.2	76	18	AAT92339 Ribozyme (15) to s
C 43	23	1.2	77	22	ABA74315 Human foetal liver
C 44	23	1.2	77	22	AAK22782 Human brain expres
C 45	23	1.2	77	22	AAK48950 Human bone marrow

ALIGNMENTS

RESULT 1
ABX55459/c
ID ABX55459 standard; cDNA; 88 BP.
XX AC ABX55459;
XX
XX
DT 26-FEB-2003 (first entry)
XX
XX
DE Bovine EST associated with lactation/muscle/fat deposition #5388.
XX
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
XX
OS Bos Taurus.
XX
XX
PN US2002137160-A1.
XX
XX
PD 26-SEP-2002.
XX
XX
PF 26-OCT-2001; 2001US-0983965.
XX
XX
PR 17-DEC-1998; 98US-113678P.
PR 15-DEC-1999; 99US-0465231.
XX
XX
PA (BYATT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
XX
PI Byatt JC, Mathialagan N, Tao N, Warren WC;

CC (ABZ78294-ABZ7913), which are involved in the molecular pathways of
CC tumour suppression, tumour reversion, apoptosis and/or virus resistance.
CC The sequences are also useful for treatment or prevention of viral,
CC tumour and cell degenerative diseases, and also for diagnosis and
CC prognosis of these diseases.
CC Note: The sequence data for this patent is not represented in the
CC printed specification but is based on sequence information supplied
CC by the European Patent Office.

XX
SQ Sequence 94 BP; 29 A; 17 C; 17 G; 31 T; 0 other;
Query Match 1.3%; Score 25; DB 25; Length 94;
Best Local Similarity 56.8%; Pred. No. 8.2e+03;
Matches 46; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1646 TTTAATTTTGCATTTATTATGACCATAGGATTCCTCTAGGAACCTTTATCGTCTCTTTAT 1705
Db 85 TTCAATTTTAAATACACACACAGTAGGAAGTACACTGGCAGCTGTAAACATGCTCTGTAT 26

QY 1706 ATGCACCACTCTGTTGTTG 1726
Db 25 ATACACACAGTATGCTAG 5

RESULT 4
ABZ09133/C
ID ABZ09133 standard; DNA; 94 BP.
XX
AC ABZ09133;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human oligonucleotide SEQ ID 293.
XX
KW Human; tumour suppressor; virucide; cytostatic; nootropic;
KW neuroprotective; neuroleptic; gene therapy; tumour suppression;
KW tumour reversion; apoptosis; viral resistance; viral infection;
KW cell degeneration; Alzheimer's disease; schizophrenia; cancer; ds.
XX
OS Homo sapiens.
XX
PN FR2822475-A1.
XX
PD 27-SEP-2002.
XX
PF 20-MAR-2002; 2002FR-0003459.
XX
PR 13-FEB-2001; 2001FR-0001925.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Telerman A, Amson R, Tuijnder M, Susini L;
XX
DR WPI; 2003-032204/03.
XX
PT New human nucleic acid, useful for diagnosis, prognosis and treatment,
PT e.g. of tumors, also related vectors, transformed cell, polypeptides
PT and antibodies -
XX
PS Disclosure; Page 82; 189pp; French.
XX
CC The present invention relates to human oligonucleotides
CC (ABZ08941-ABZ09860). The expression of the oligonucleotides is implicated
CC in tumour suppression or reversion, apoptosis and/or viral resistance.
CC The oligonucleotides are useful for preventing and/or treating viral
CC infection, tumour development and cell degeneration (e.g. Alzheimer's
CC disease and schizophrenia), especially cancer.
XX
SQ Sequence 94 BP; 29 A; 17 C; 17 G; 31 T; 0 other;
Query Match 1.3%; Score 25; DB 25; Length 94;
Best Local Similarity 56.8%; Pred. No. 8.2e+03;
Matches 46; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1646 TTTAATTTTGCATTTATTATGACCATAGGATTCCTCTAGGAACCTTTATCGTCTCTTTAT 1705
Db 85 TTCAATTTTAAATACACACACAGTAGGAAGTACACTGGCAGCTGTAAACATGCTCTGTAT 26

QY 1706 ATGCACCACTCTGTTGTTG 1726
Db 25 ATACACACAGTATGCTAG 5

RESULT 5
ABA82853/C
ID ABA82853 standard; DNA; 90 BP.
XX
AC ABA82853;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human protective DNA sequence CNI-00746 fragment #18.
XX
KW Human; protective sequence; cell death; cancer; autoimmune disease;
KW neurological disorder; stroke; cytostatic; neuroprotective; gene therapy;
KW ds.
XX
OS Homo sapiens.
XX
PN WO200176457-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11663.
XX
PR 11-APR-2000; 2000US-0547735.
XX
PA (COGE-) COGENT NEUROSCIENCE INC.
XX
PI Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC, Barney S;
XX
DR WPI; 2002-025874/03.
DR P-PSDB; ABB44754.
XX
PT New protective sequences and their products, useful for diagnosing and
PT treating diseases involving cell death, including neurological
PT disorders e.g. stroke and for identifying modulators of expression of
PT the protective sequences -
XX
PS Claim 2; Fig 11; 283pp; English.
XX
CC The present invention relates to protective sequence proteins
CC (ABB44624-ABB44830) and their coding sequences (ABA82701-ABA82937).
CC The sequences, when introduced into a cell either predisposed to undergo
CC cell death or in the process of undergoing cell death, prevent, delay or
CC rescue the cell from death, hence, these sequences are named "protective
CC sequences". The sequences are useful for treating and/or ameliorating
CC cancer, autoimmune diseases and neurological disorders e.g. stroke.
CC Further examples of diseases which may be treated by the present
CC invention are given in the specification.
XX
SQ Sequence 90 BP; 29 A; 19 C; 11 G; 31 T; 0 other;
Query Match 1.3%; Score 24.4; DB 24; Length 90;
Best Local Similarity 60.6%; Pred. No. 1.2e+04;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 713 ACTAAATTTTTCATGCTGTGGATGAATAGACCCACATACACAGTTGCATATGATG 772
Db 74 AATATGTTGTTTTCATTGGAGTATATGAAGAAACCCAGCTTAAAGAGTTATGTAGTGG 15

QY 773 AATAAG 778
Db 14 AAAAAG 9

RESULT 6

AA07251
ID AAX07251 standard; DNA; 95 BP.

XX AC AAX07251;

XX DT 20-MAR-2003 (updated)

XX DT 21-MAY-1999 (first entry)

XX Genetic suppressor element CF-313 used to inhibit HIV infection.

XX CF-313; genetic suppressor element; GSE; HIV; infection; AIDS;

KW therapy; protein tyrosine kinase; human; ss.

XX OS Homo sapiens.

XX PN WO9854366-A1.

XX PD 03-DEC-1998.

XX XX 02-JUN-1998; 98WO-US11452.

XX PF 02-JUN-1997; 97US-0867314.

XX PR 29-MAY-1998; 98US-0087809.

XX XX (SUBS-) SUBSIDIARY NO 3 INC.

XX PA Dayn A, Dunn SJ, Holzmayer TA;

XX PI WPI; 1999-070224/06.

XX DR

XX XX

XX PT Composition for inhibiting human immunodeficiency virus - containing

XX PT either fragments of cellular genes that express proteins essential

XX PT for productive infection, or inhibitors of these cellular gene

XX PT products

XX XX

XX PS Claim 23; Page 60; 85pp; English.

XX CC

XX CC This is the nucleotide sequence of genetic suppressor element (GSE)

XX CC CF-313, which was selected for its ability to prevent productive

XX CC infection of CEM-s cells by HIV. It has substantial sequence

XX CC identity with the gene encoding human protein tyrosine phosphatase.

XX CC The invention relates to compositions and methods for inhibiting

XX CC HIV infection by down-regulating the expression and/or function of

XX CC certain human cellular genes. 20 GSEs (see AAX07239-58) are provided

XX CC that correspond to, or are complementary to, a portion of a

XX CC cellular gene and which encode intracellular products which are

XX CC necessary for a productive HIV infection. Some of the selected

XX CC GSEs function in the sense orientation, possibly as transdominant

XX CC mutants or RNA decoys. Other GSEs function in the antisense

XX CC orientation, and may exert their effects as antisense RNA. The

XX CC GSEs are used to protect cells against HIV infection, either in

XX CC vitro (e.g. introduced into haematopoietic cells before these are

XX CC used for engraftment) or in vivo, by direct transduction, e.g.

XX CC using a gene therapy vector. A method is also provided for

XX CC identifying additional cellular genes as therapeutic targets for

XX CC suppressing HIV infection.

XX CC (Updated on 20-MAR-2003 to correct PR field.)

XX XX

XX SQ Sequence 95 BP; 28 A; 15 C; 13 G; 39 T; 0 other;

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RESULT 7

AAF93098
ID AAF93098 standard; CDNA; 95 BP.

XX AC AAF93098;

XX DT 22-MAY-2001 (first entry)

XX XX Human HIV/tumorigenesis genetic suppressor element, SEQ ID NO:13.

XX DE HIV infection; tumorigenesis; inhibition; genetic suppressor element;

XX KW GSE; human cellular gene expression inhibitor; transdominant mutant;

XX KW RNA decoy; antisense; anti-HIV; anticancer; ss.

XX XX Homo sapiens.

XX PN WO200116323-A2.

XX PD 08-MAR-2001.

XX PF 01-SEP-2000; 2000WO-US24353.

XX PR 01-SEP-1999; 99US-0388184.

XX XX (SUBS-) SUBSIDIARY NO 3 INC.

XX PA Holzmayer TA, Dunn SJ;

XX PI WPI; 2001-235108/24.

XX DR

XX XX

XX PT Inhibitory composition for preventing tumorigenesis, comprises a

XX PT cell-derived nucleic acid molecule, referred to as a genetic suppressor

XX PT element, a cell-derived protein or an inhibitor of a product of a

XX PT target gene

XX XX

XX PS Example 1; Page 92; 121pp; English.

XX CC

XX CC The invention relates to compositions and methods for inhibiting HIV

XX CC infection and tumorigenesis by downregulating the expression of certain

XX CC human cellular genes, and/or inhibiting the activity of products encoded

XX CC by such genes. In particular, the invention relates to a number of human

XX CC cell-derived nucleic acid molecules which inhibit tumorigenesis or HIV

XX CC infection in susceptible cells. These nucleic acid molecules, designated

XX CC genetic suppressor elements (GSEs; AAF93086-AAF93177), correspond to

XX CC portions of cellular genes or complements thereof. The GSEs in the

XX CC sense orientation exert their effects as transdominant mutants or

XX CC RNA decoys, while the GSEs in the antisense orientation act as antisense

XX CC RNA. The invention also encompasses anti-tumorigenic compositions

XX CC comprising an isolated cell-derived protein or a mimotope thereof, or an

XX CC inhibitor of a product of a target gene identified by its ability to

XX CC inhibit tumour cell formation. The present sequence represents a human

XX CC GSE described in an exemplification of the invention.

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XX SQ Sequence 95 BP; 28 A; 15 C; 13 G; 39 T; 0 other;

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RESULT 8

AAF94529
ID AAF94529 standard; DNA; 95 BP.

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AC AAF94529;
XX
XX DT 22-MAY-2001 (first entry)
XX DE
XX Genetic suppressor element DNA sequence CF-313.
XX
XX KW Genetic suppressor element; GSE; human immunodeficiency virus; HIV;
XX infection inhibitor; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200116322-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 01-SEP-2000; 2000WO-US24262.
XX
XX PR 01-SEP-1999; 99US-0388182.
XX
XX PA (SUBS-) SUBSIDIARY NO 3 INC.
XX
XX PI Holzmayer TA, Dunn SJ;
XX
XX WP1; 2001-235107/24.
XX
XX CC New isolated genetic suppressor element nucleic acid molecule encoding
XX protein such as bone morphogenic protein-1, and double-strand break DNA
XX repair gene protein, for treating human immunodeficiency virus
XX infection -
XX
XX Example 1; Page 91; 106pp; English.
XX
XX CC Polynucleotide sequences AAF94517 - AAF94536 and AAF94539 - AAF94574
XX represent genetic suppressor element (GSE) nucleic acid molecules which
XX share homology to fragments of genes. When the GSE is operably linked to
XX a regulatory sequence, expression of the GSE in a host cell inhibits
XX infection by human immunodeficiency virus (HIV). The GSE sequences work
XX in gene therapy as human cellular gene product inhibitors or mRNA
XX translation blockers. A composition comprising a protective compound
XX selected from a polypeptide encoded by the GSE sequence, its mimotope,
XX GSE, and an inhibitor of a product of a target gene is useful for
XX protecting host cells from HIV infection by introducing and for treating
XX HIV infection. The GSE sequences are useful for the design of
XX polypeptides or peptides capable of inhibiting HIV infection.
XX
XX SQ Sequence 95 BP; 28 A; 15 C; 13 G; 39 T; 0 other;
XX
XX Query Match 1.3%; Score 24.4; DB 22; Length 95;
XX Best Local Similarity 58.1%; Pred. No. 1.2e+04;
XX Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
XX
XX QY 791 AAGCATGATTTCTTGAGAGATGCAAAAACCTTTGGCGTGTCTCTGGAAGTGTTCCTT 850
XX Db 14 AAGGATGACTTTTATACAAATGGAATAAATTATGCGATTTCTTATTGAAATTTCAACGCT 73
XX
XX QY 851 TTAGGTTGCGTTCG 864
XX Db 74 TTGTTTCTTTGGC 87
XX
XX RESULT 9
XX ABT03434
XX ID ABT03434 standard; DNA; 95 BP.
XX
XX AC ABT03434;
XX
XX DT 03-OCT-2002 (first entry)
XX
XX DE Human HIV-inhibiting genetic suppressor element (GSE) 13.
XX
XX KW Human; GSE; genetic suppressor element; ds; HIV inhibition; HIV;
XX HIV biological pathway; HIV inhibitor.
XX
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OS Homo sapiens.
XX
XX PN WO200244722-A2.
XX
XX PD 06-JUN-2002.
XX
XX PF 28-NOV-2001; 2001WO-US44463.
XX
XX PR 28-NOV-2000; 2000US-0724916.
XX
XX PA (SUBS-) SUBSIDIARY NO 3.
XX
XX PI Holzmayer TA, Dunn SJ;
XX
XX WP1; 2002-537469/57.
XX
XX PT Identifying pathways involved in HIV infection, by transferring a
XX fragment library produced from polynucleotide encoding a protein of the
XX pathway into cells and selecting cells having down-regulated latent HIV
XX genes -
XX
XX Example 1; Page 97; 114pp; English.
XX
XX CC The invention comprises compositions and methods for inhibiting HIV
XX infection by down-regulating expression of certain human cellular genes
XX and/or inhibiting the activity of the products encoded by such genes. The
XX invention particularly relates to genetic suppressor elements (GSEs) -
XX nucleic acid sequences which inhibit HIV infection. The GSEs correspond
XX to portions of cellular genes which encode intracellular products that
XX are necessary for productive HIV infection. The compositions and methods
XX of the invention are useful for identifying a biological pathway involved
XX in HIV infection and for identifying a compound as an HIV inhibitor. The
XX present DNA sequence represents a human GSE of the invention.
XX
XX SQ Sequence 95 BP; 28 A; 15 C; 13 G; 39 T; 0 other;
XX
XX Query Match 1.3%; Score 24.4; DB 24; Length 95;
XX Best Local Similarity 58.1%; Pred. No. 1.2e+04;
XX Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
XX
XX QY 791 AAGCATGATTTCTTGAGAGATGCAAAAACCTTTGGCGTGTCTCTGGAAGTGTTCCTT 850
XX Db 14 AAGGATGACTTTTATACAAATGGAATAAATTATGCGATTTCTTATTGAAATTTCAACGCT 73
XX
XX QY 851 TTAGGTTGCGTTCG 864
XX Db 74 TTGTTTCTTTGGC 87
XX
XX RESULT 10
XX ABN57082
XX ID ABN57082 standard; DNA; 65 BP.
XX
XX AC ABN57082;
XX
XX DT 15-JUL-2002 (first entry)
XX
XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:29830.
XX
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX OS Mus musculus.
XX
XX PN WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB01903.
XX
XX PR 28-JUL-2000; 2000US-221607P.
XX
XX PA 02-MAY-2001; 2001US-287724P.
XX
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(COMP-) COMPUEN INC.
Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
WPI, 2002-257383/30.
New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -
Example 1; SEQ ID 29830; 47pp; English.
The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Sequence 65 BP; 14 A; 12 C; 17 G; 22 T; 0 other;
Query Match 1.3%; Score 24.2; DB 24; Length 65;
Best Local Similarity 66.0%; Pred. No. 1.1e+04;
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Qy 816 AAAAAGTTGGCTGTTCTGGAAGTGTCTTTCTTTAGTGGCTGCTCTC 868
Db 13 AAAGAATTGGCTGGATTGTTGTTGAGTATCCCAATTAGATGTTCTGCTGC 65
RESULT 11
AAT26550/c
ID AAT26550 standard; cDNA to mRNA; 97 BP.
XX AAT26550;
XX 10-OCT-1996 (first entry)
XX Human gene signature HUMGS08795.
XX Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
XX Homo sapiens.
XX WO9514772-A1.
XX 01-JUN-1995.
XX 11-NOV-1994; 94WO-JP01916.
XX 12-NOV-1993; 93JP-0355504.
XX

(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
WPI, 1995-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues
Claim 1; Page 2114; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
Sequence 97 BP; 35 A; 8 C; 12 G; 41 T; 1 other;
Query Match 1.3%; Score 24.2; DB 16; Length 97;
Best Local Similarity 62.3%; Pred. No. 1.4e+04;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1395 ATTTCTTTTGAAGAAAATTCAAATAGATTTGCAAGCCATTGGTCTTTAATGACTGTAT 1454
Db 75 ATTTATTGCAGAAAATATACAAAGATATTTTACAAAACAATCAATAAATATGATGCAT 16
Qy 1455 T 1455
Db 15 T 15
RESULT 12
AAK68002/c
ID AAK68002 standard; DNA; 97 BP.
XX AAK68002;
XX 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22814.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX

PR	19-MAY-2000;	2000US-02055515;
PR	27-JUN-2000;	2000US-02049467;
PR	28-JUN-2000;	2000US-02118866;
PR	30-JUN-2000;	2000US-0215135;
PR	07-JUL-2000;	2000US-0216647;
PR	07-JUL-2000;	2000US-0216880;
PR	11-JUL-2000;	2000US-0217487;
PR	11-JUL-2000;	2000US-0217496;
PR	14-JUL-2000;	2000US-0218290;
PR	26-JUL-2000;	2000US-0220963;
PR	26-JUL-2000;	2000US-0220964;
PR	14-AUG-2000;	2000US-0224518;
PR	14-AUG-2000;	2000US-0224519;
PR	14-AUG-2000;	2000US-0225214;
PR	14-AUG-2000;	2000US-0225214.3;
PR	14-AUG-2000;	2000US-0225266;
PR	14-AUG-2000;	2000US-0225267;
PR	14-AUG-2000;	2000US-0225268;
PR	14-AUG-2000;	2000US-0225270;
PR	14-AUG-2000;	2000US-0225447;
PR	14-AUG-2000;	2000US-0225575;
PR	14-AUG-2000;	2000US-0225758;
PR	14-AUG-2000;	2000US-0225759;
PR	18-AUG-2000;	2000US-0226279;
PR	22-AUG-2000;	2000US-0226868;
PR	22-AUG-2000;	2000US-0227182;
PR	23-AUG-2000;	2000US-0227009;
PR	30-AUG-2000;	2000US-0228924;
PR	01-SEP-2000;	2000US-0229287;
PR	01-SEP-2000;	2000US-0229343;
PR	01-SEP-2000;	2000US-0229344;
PR	01-SEP-2000;	2000US-0229345;
PR	05-SEP-2000;	2000US-0229509;
PR	05-SEP-2000;	2000US-0229531;
PR	06-SEP-2000;	2000US-0230437;
PR	06-SEP-2000;	2000US-0230438;
PR	08-SEP-2000;	2000US-0231242;
PR	08-SEP-2000;	2000US-0231243;
PR	08-SEP-2000;	2000US-0231244;
PR	08-SEP-2000;	2000US-0231413;
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PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-)	HUMAN GENOME SCI INC.
XX		
XX		
PI	Rosen CA,	Barash SC, Ruben
PI	WPI;	2001-483426/52.
XX		
XX		
PT	Nucleic acids encoding human	
PT	useful for preventing, diagnosing	
PT	metastasis -	
XX		
XX		
PS	Disclosure;	SEQ ID NO 22814;
XX		
XX		
CC	AAK54951 to AAK64702 encode the	
CC	amino acid sequences given in	
CC	activity, and can be used in	
CC	proteins and polynucleotides	
CC	coding and polynucleotides	

KW altered culture condition; environmental stress;
KW physiological provocation; ds.

XX Bacillus licheniformis.

XX WO200229113-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US31437.

XX 06-OCT-2000; 2000US-0680598.

XX 27-MAR-2001; 2001US-279526P.

XX (NOVO) NOVOZYMES BIOTECH INC.

XX (NOVO) NOVOZYMES AS.

XX Berka R, Clausen IG;

XX WPI; 2002-416684/44.

XX Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second
PT Bacillus cells, by using substrate containing Bacillus genomic
PT sequenced tag array

XX Claim 4; SEQ ID NO 3986; 200pp; English.

CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC a relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive
CC follow-up characterisation is unnecessary, when one spot on an array
CC equals one gene or one open reading frame, since sequence information is
CC available. This sequence represents a genomic sequence tag (GST) used in
CC the method of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 87 BP; 15 A; 18 C; 25 G; 29 T; 0 other;

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Db 1 GAGCGGAGGTGTACGGACACGGAAGCGGTTTGCTTTAATTGTTGTTCTGTTCTATTCTTT 60

QY 391 GCTTATC 397

Db 61 AATCATC 67

RESULT 20

AAS41939/c

ID AAS41939 standard; DNA; 89 BP.

XX

AC AAS41939;

XX

DT 17-DEC-2001 (first entry)

XX Genomic sequence #255 encoding novel human enzyme polypeptide.

XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotropic; anticoagulant; ds.

XX Homo sapiens.

XX WO200155301-A2..

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01239.

XX 31-JAN-2000; 2000US-0179065.

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PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465566/50.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
XX preventing, treating neural, immune system, muscular, reproductive,
XX pulmonary, cardiovascular, renal, proliferative disorders and cancerous
XX diseases -
XX
XX Disclosure; SEQ ID No 2065; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
XX polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
XX encoding them. The enzyme polypeptides of the invention may comprise the
XX functional classes of oxidoreductases, transferases, hydrolases, lyases,
XX isomerases or ligases. The sequences of the invention are useful in the
XX diagnosis, treatment, prevention and/or prognosis of a wide range of
XX disorders including hyperproliferative disorders (e.g. cancer),
XX immunodeficiency disorders (e.g. AIDS) autoimmune disorders
XX (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
XX metabolic disorders (e.g. phenylketonuria), inflammatory disorders
XX (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
XX blood-related disorders (e.g. haemophilia), reproductive disorders
XX (e.g. infertility) and infectious disorders (e.g. influenza). The
XX polynucleotides of the invention can also be used in gene therapy.
XX AAS41685-AAS42192 represent DNA sequences encoding for the novel human
XX enzyme polypeptides of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
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XX Sequence 89 BP; 33 A; 22 C; 23 G; 11 T; 0 other;
XX
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XX Best Local Similarity 55.4%; Fred. No. 1.7e+04;
XX Matches 46; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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Db 86 TTTTCCTTTTTCGACAGAGTCTCACTCTGTTGCCAGGCTGAGTGGTGGATC 27
QY 901 GGATTTTAAAGGAGGTATGCTT 923
Db 26 TTGGCTCACTGCAGCCTCTGCT 4
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RESULT 21
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ID AAS41952 standard; DNA; 89 BP.
XX
AC AAS41952;
XX
XX 17-DEC-2001 (first entry)
XX
XX Genomic sequence #268 encoding novel human enzyme polypeptide.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
XX ligase; hyperproliferative disorder; immunodeficiency disorder;
XX autoimmune disorder; neurological disorder; metabolic disorder;
XX inflammatory disorder; cardiovascular disorder; reproductive disorder;
XX blood-related disorder; infectious disorder; gene therapy; cytostatic;
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KW anti arthritic; nephrotropic; anticoagulant; ds.
XX
OS Homo sapiens.
XX WO200155301-A2.
PN
XX
PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01239.
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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-0254978.

PR 22-AUG-2001; 2001US-314050P.
XX (ELIT-) ELITRA PHARM INC.
PA Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
PI WPI; 2002-566694/60.
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
PT expression
XX
XX Claim 76; SEQ ID NO 3029; 167pp + Sequence Listing; English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX
XX Sequence 65 BP; 21 A; 7 C; 18 G; 19 T; 0 other;
SQ
Query Match 1.3%; Score 23.6; DB 24; Length 65;
Best Local Similarity 69.6%; Pred. No. 1.7e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 268 AAAACAATGTACACAGGCATTATCTCAGCATGCTGTGGCTGGCA 313
DB 19 AAAGCAATGTATAAAGGCTTGGTATAAGGATGGTGTACATTAGCA 64
RESULT 24
AAC11402
ID AAC11402 standard; cDNA; 79 BP.
XX
AC AAC11402;
XX
XX 06-OCT-2000 (first entry)
DT
DE Human secreted protein 5' EST, SEQ ID NO: 15477.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW Gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
OS
XX EP1033401-A2.
PN
XX 06-SEP-2000.
PD
XX 21-FEB-2000; 2000EP-0200610.
PF
XX

PR 26-FEB-1999; 99US-0122487.
XX (GEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
PT expression
XX
XX Claim 1; SEQ ID 15477; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
XX Sequence 79 BP; 22 A; 11 C; 14 G; 32 T; 0 other;
SQ
Query Match 1.3%; Score 23.6; DB 21; Length 79;
Best Local Similarity 69.6%; Pred. No. 1.8e+04;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1348³ TTTAATTCATGACCTTTGGTACCTGTGCAGTCTGTGTTATAGCA 1393
DB 3 TTTAATTCATGATGTTATCTCTCTGGAGATAGTTATAGAA 48
RESULT 25
AAS23666
ID AAS23666 standard; DNA; 90 BP.
XX
AC AAS23666;
XX
XX 04-DEC-2001 (first entry)
DT
XX
XX Tetracycline promoter downstream PCR primer (Tet-Down) #41.
XX
XX Gene identification; essential gene; GRACE; pathogenic fungus;
KW Gene replacement and conditional expression; fungal infection;
KW PCR primer; Tet-down; tetracycline promoter; ss.
XX
XX Escherichia coli.
OS
XX Candida albicans.
XX
XX WO200160975-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 20-FEB-2001; 2001WO-US05551.
PF
XX 18-FEB-2000; 2000US-0183534.
PR
XX (ELIT-) ELITRA PHARM INC.
PA
XX Roemer T, Jiang B, Boone C, Bussey H;
PI WPI; 2001-489080/53.
XX
XX Identifying genes essential to fungal metabolisms and identifying
PT potential therapeutic agents that target these genes -
PT

CC ligation reaction mixture. The reaction mixture is subjected to a cycle
CC of ligation, where adjacently hybridising complementary probes are
CC ligated to one another to form a ligation product. The mixture is then
CC combined with a primer set including a primer comprising a reporter
CC group, and a polymerase to make an amplification mixture. The target
CC sequences can then be detected via the reporter group. The method is
CC useful for identifying splice variants. Sequences ABK17220-ABK17313
CC represent probes and PCR primers used in the method of the invention.
XX

SQ Sequence 98 BP; 23 A; 15 C; 20 G; 40 T; 0 other;

Query Watch . 1.3%; Score 23.6; DB 24; Length 98;
Best Local Similarity 58.6%; Pred. No. 2e+04; Mismatches 0; Gaps 0;
Matches 41; Conservative 0; Indels 29; Gaps 0;

QY 1156 TGTGAGAAACAGCGCTTAGATTCTTCTACGGAAACTCTTAACGAAACGCCAAAATTTTGTC 1215
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 77 TGTGAGNAACAGCCATGTATCATATACGGCAATCAATAAGGAAC TTATGACCTAAAGC 18

QY 1216 AAAGGTAAGC 1225
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 17 AAAGGTA AAC 8

RESULT 27
ABK17305
ID ABK17305 standard; DNA; 98 BP.
XX
AC ABK17305;
XX
DT 26-MAR-2002 (first entry)
XX
DE Coupled ligation and amplification oligonucleotide #86.
XX Human; coupled ligation and amplification reaction; probe; PCR primer;
KW splice variant; ss.
XX Homo sapiens.
OS
XX WO2001192579-A2.
PN
XX PD 06-DEC-2001.
PD
XX PF 30-MAY-2001; 2001WO-USU17329.
PF
XX PR 30-MAY-2000; 2000US-0584905.
PR
XX PR 28-NOV-2000; 2000US-0724755.
PR
XX PA (PEKE) PE CORP NY.
PA
XX PI Wenz H, ⁶ Schroth GP;
PI
XX PFI WPI; 2002-114362/15.
F1
XX
XX Detecting target nucleic acids for identifying splice variants in a
PT target nucleic acid sequence, comprises utilising coupled-ligation and
PT amplification -
PT
XX Disclosure; Page 117; 119pp; English.

XX The invention relates to detecting target sequences in a sample by
XX utilising a coupled ligation and amplification reaction. The method
XX involves combining the sample with a probe set for each target sequence,
XX the probe set comprising a probe comprising a target-specific portion
XX ('TSP') and a 5' primer-specific portion or TSP alone, and another probe
XX comprising a TSP and a 3' primer-specific portion, where the probes in
XX each set are suitable for ligation together when hybridised adjacent to
XX one another on a complementary target sequence. At least one probe in
XX each probe set further comprises an addressable support-specific portion
XX located between the primer-specific portion and the TSP to form a
XX ligation reaction mixture. The reaction mixture is subjected to a cycle
XX of ligation, where adjacently hybridising complementary probes are
XX ligated to one another to form a ligation product. The mixture is then

Db	28	CCCTATAGTG 19	88	TTTCTCTCTGTGAAGAGGTGATGGTGATGGTGATGCATTGTAATTGTTAAATAGTAATTGT 29
Db	685	CTCTTCAATG 694		
Db	28	CCCTATAGTG 19		
RESULT 31				
ABN32824				
ID	ABN32824	standard; DNA; 60 BP.		
AC	ABN32824;			
DT	30-JUL-2002	(first entry)		
DE	Human 10 Fn3 gene related oligonucleotide SEQ ID NO:5.			
XX	Protein scaffold; antibody; binding protein; immunoglobulin;			
KW	tumour necrosis factor alpha; TNF-alpha; protein framework; primer; ss.			
OS	Homo sapiens.			
OS	Synthetic.			
XX	WO200232925-A2.			
PN				
PD	25-APR-2002.			
XX				
PF	16-OCT-2001; 2001WO-US32233.			
XX				
PR	16-OCT-2000; 2000US-0688566.			
XX	(PHYL-) PHYLUS INC.			
PA				
PI	Lipovsek D, Wagner RW, Kuimelis RG;			
XX				
DR	WPI; 2002-444238/47.			
XX				
PT	New non-antibody proteins having an immunoglobulin fold, useful in			
PT	research, therapeutic or diagnostic fields, particularly as scaffolds			
PT	for designing proteins with specific properties, e.g. for binding any			
PT	antigen of interest			
XX				
PS	Disclosure; Page 30; 94pp; English.			
XX				
CC	The present invention describes a non-antibody protein, comprising a			
CC	domain having an immunoglobulin-like fold, derived from a reference			
CC	protein having a mutated amino acid sequence, where the non-antibody			
CC	protein binds with a Kd at least as tight as 10 nM to a compound that			
CC	is not bound as tightly by the reference protein. The non-antibody			
CC	protein is useful as scaffolds for selecting or designing a protein			
CC	framework with specific and favourable properties, e.g. for binding any			
CC	antigen of interest, or for destroying or inactivating antibody			
CC	molecules. The non-antibody protein is also useful in all areas where			
CC	antibodies are used, e.g. research, therapeutic or diagnostic fields,			
CC	and for screening novel binding proteins useful in the above-mentioned			
CC	fields. The present proteins have thermodynamic properties superior to			
CC	those of natural antibodies, and can be evolved rapidly in vitro. The			
CC	present proteins or antibody mimics exhibit improved biophysical			
CC	properties, such as stability under reducing conditions and solubility			
CC	at high concentrations. In addition, these molecules are readily			
CC	expressed and folded in prokaryotic systems (e.g. Escherichia coli), in			
CC	eukaryotic systems (e.g. yeast), or in vitro translation systems			
CC	(e.g. rabbit reticulocyte lysate system). Furthermore, these proteins			
CC	are extremely amenable to affinity maturation techniques involving			
CC	multiple cycles of selection, e.g. in vitro selection using RNA-protein			
CC	fusion technology, phage display or yeast display systems. The present			
CC	sequence is used in the exemplification of the present invention.			
XX				
SQ	Sequence 99 BP; 33 A; 28 C; 13 G; 25 T; 0 other;			
Query Match	1.3%; Score 23.6; DB 24; Length 99;			
Best Local Similarity	58.6%; Pred. No. 2e+04;			
Matches	41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;			
QY	625 TTTCTCTCTAGTACAGGCGCTTAAAGGGTTGCTTTGACATGATTTTGGAAATTTT 684			

Query Match 1.3%; Score 23.4; DB 24; Length 60;
Best Local Similarity 67.3%; Pred. No. 1.8e+04;

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Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 118 TTTAAAGTCCCAATTCGAAATATCATGCCAGTGTCTCAGGGAATTTACC 166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TTTACCTTCAAGTTTCAAGTTTCATGCTACTGTCTCAGAGAGGTTTCC 50

RESULT 32
AAC53034/C
ID AAC53034 standard; DNA; 78 BP.
XX
AC AAC53034;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 73179.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000BP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134321.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
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PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.

Query Match 1.3%; Score 23.4; DB 21; Length 78;
Best Local Similarity 53.4%; Pred. No. 2e+04;
Matches 39; Conservative 4; Mismatches 30; Indels 0; Gaps 0;
QY 1204 AAATTTTGGCTCAAGTACGACCAAACTATCGAAGAAAATCGGTATATCAGCGGACCAT 1263
DB 77 AATATTTTTCAGAGAGAAAGAGACTTTATATATAATTAAGTAAGAAGAGATTGA 18
QY 1264 CGGCTTTTAGGA 1276

Db 17 GAGRAATWTAKGA 5
RESULT 33
AAK69024/c
ID AAK69024 standard; DNA; 84 BP.
XX
AC AAK69024;
XX
DT 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23836.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.

```
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PR 14-SEP-2000; 2000US-0232398.
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PR 14-SEP-2000; 2000US-0233064.
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PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
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PR 02-OCT-2000; 2000US-0237037.
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PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.

PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 23836; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 84 BP; 27 A; 20 C; 23 G; 14 T; 0 other;
SQ

Query Match 1.3%; Score 23.4; DB 22; Length 84;
Best Local Similarity 55.6%; Pred. No. 2.1e+04;
Matches 45; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 843 TTTTCTTTTAGGTGGTGTCTCTCGGGTTGGAGCTCGAATTCGGTTTGGGAATGG 902
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 TTTTCTTTTAGGTGGAGCTCTCTCTGTGTCCAGGCTGGAGTGCAGTCAATCTC 25
QY 903 ATTTTAAAGGAGGATGCCT 923
Dy 24 AGCTCACTGCAAGCTCTGCCT 4

RESULT 34
AAT21076/c
ID AAT21076 standard; cDNA to mRNA; 87 BP.
XX AAT21076;
XX
XX 16-JUL-1996 (first entry)
XX Human gene signature HUMGS02361.
XX
XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
```


DR WPI; 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and

PT developmental-specific genes

XX

PS Example 1; SEQ ID 18757; 47pp; English.

XX

CC The present invention describes oligonucleotide libraries for detecting

CC messenger RNAs that populate a (sub-)transcriptome, where the

CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises

CC several oligonucleotides, each capable of hybridising selectively to a

CC set of messenger RNAs transcribed from a given transcription unit of

CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or

CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal

CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a

CC particular biological or pathological state, and so allowing the

CC detection of tissue- and pathology-specific genes such as those genes

CC only expressed in specific tissue under a specific pathological

CC condition; to detect developmental specific genes; and to detect RNA

CC transcripts and splice variants of a transcriptome of a patient suffering

CC from a particular disorder. ABN27253 to ABN59589 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in

CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

QQ Sequence 60 BP; 10 A; 10 C; 20 G; 20 T; 0 other;

XX

Query Match 1.2%; Score 23.2; DB 24; Length 60;

Best Local Similarity 70.5%; Pred. No. 2.1e+04;

Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 604 AGTATTGGCTCAGCACTCTTTCTTCTTCTAGATACAGGCGCTTA 647

DB 11 AGGAATGGCTCAGCTCTTTTGTCTGCTGCTTTTGGGGCCA 54

RESULT 37

ABN49485/c

ID ABN49485 standard; DNA; 60 BP.

XX

AC ABN49485;

XX

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:22233.

DE Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

KW

OS Homo sapiens.

OS

XX WO200210449-A2.

XX

PN 07-FEB-2002.

XX

PD 20-JUL-2001; 2001WO-IB01903.

XX

PF 28-JUL-2000; 2000US-221607P.

XX

PR 02-MAY-2001; 2001US-287724P.

XX

XX (COMP-) COMPUGEN INC.

PA Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

PI

XX

DR WPI; 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and

PT developmental-specific genes

XX

PS Example 1; SEQ ID 22233; 47pp; English.

XX

CC The present invention describes oligonucleotide libraries for detecting

CC messenger RNAs that populate a (sub-)transcriptome, where the

CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises

CC several oligonucleotides, each capable of hybridising selectively to a

CC set of messenger RNAs transcribed from a given transcription unit of

CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or

CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal

CC transcriptomes. The libraries may also be used as specialised mini

CC libraries to detect transcripts of a sub-transcriptome under a

CC particular biological or pathological state, and so allowing the

CC detection of tissue- and pathology-specific genes such as those genes

CC only expressed in specific tissue under a specific pathological

CC condition; to detect developmental specific genes; and to detect RNA

CC transcripts and splice variants of a transcriptome of a patient suffering

CC from a particular disorder. ABN27253 to ABN59589 represent

CC oligonucleotide sequences from rats, humans and mice, which are used in

CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

QQ Sequence 60 BP; 16 A; 13 C; 17 G; 14 T; 0 other;

XX

Query Match 1.2%; Score 23.2; DB 24; Length 60;

Best Local Similarity 77.8%; Pred. No. 2.1e+04;

Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 995 CAGGAAGCTGGTCTTTCTTCTTCTAGAGACTTCGCTATT 1030

DB 46 CAGGACGCTGCTCTTTGGGCTTGAGACTTCCTTACT 11

RESULT 38

AAA96467

ID AAA96467 standard; DNA; 70 BP.

XX

AC AAA96467;

XX

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of the directional building block S1.

DE

XX petE promoter; chimeric promoter; transgenic plant; MPr1108;

KW plastocyanin gene promoter; ss.

KW

OS Synthetic.

OS

XX WO200056906-A1.

XX

PN 28-SEP-2000.

XX

PD 20-MAR-2000; 2000WO-IB00317.

XX

PF 22-MAR-1999; 99FR-0003635.

XX

PR (MERI-) MERISTEM THERAPEUTICS.

XX

PA Rance I, Gruber V, Theisen M;

XX

PI WPI; 2000-587667/55.

XX

DR

XX Chimeric expression promoter for producing dicotyledonous and
PT monocotyledonous transgenic plants comprising a nucleic acid sequence
PT derived from a promoter of the pea plastocyanin gene
XX
XX Claim 24; Page 72; 83pp; English.
XX
XX The present sequence represents the directional building block 51,
CC which is used to construct chimeric promoters of the invention. The
CC specification describes a chimeric expression promoter comprising a
CC petE promoter of the pea plastocyanin gene, or comprising a G box
CC operably or functionally linked upstream of a CAAT box, TAIIA box and
CC transcription initiation site. The chimeric promoters are used in
CC expression vectors for producing transgenic plants, such as
CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
CC species, e.g. wheat, barley, oat, rice, or corn.
XX
XX Sequence 70 BP; 26 A; 18 C; 10 G; 16 T; 0 other;
SQ
Query Match 1.2%; Score 23.2; DB 21; Length 70;
Best Local Similarity 61.7%; Pred. No. 2.2e+04;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1029 TTCAACATTTGGATCTTCAGAAAGATCAAAATCTATTATTAGTGATAAGCTTTAAGCT 1088
Db 6 TTCAACACATACAAATTCAGTAGAGAGAACTCATTACTCTTGAGAAACCTAGAGGAT 65
RESULT 39
AAC15734/c
ID AAC15734 standard; cDNA; 75 BP.
XX
XX AAC15734;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 19809.
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW Gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX EP1033401-A2.
XX 06-SEP-2000.
XX 21-FEB-2000; 2000EP-0200610.
XX 26-FEB-1999; 99US-0122487.
XX (GEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1; SEQ ID 19809; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.

CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
XX Sequence 75 BP; 19 A; 7 C; 13 G; 36 T; 0 other;
SQ
Query Match 1.2%; Score 23.2; DB 21; Length 75;
Best Local Similarity 61.7%; Pred. No. 2.3e+04;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1160 AGAAACAGCGCTAGATTTCTCTACGAAACTCTAAACGAAACGCAAAATTTGGTCAAG 1219
Db 70 AAAAAAATACATGATTTCTCTATGGATATGCACACATACCATATACTTAAAGTCAAG 11
RESULT 40
AAT65280
ID AAT65280 standard; RNA; 96 BP.
XX
XX AAT65280;
XX
XX 10-SEP-1997 (first entry)
XX Platelet derived growth factor AB binding ligand.
XX Platelet derived; growth factor; PDGF; binding ligand;
KW identification; SELEX; anti-mitogenic; inhibition; cell;
KW Systematic Evolution of Ligands by Exponential enrichment;
KW epithelial; proliferation; diagnosis; treatment;
KW neointimal lesion; arterial injury; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1..96
FT /*tag= a
FT /note= "all pyrimidines are 2'-fluoro modified"
XX
XX WO9638579-A1.
XX
XX 05-DEC-1996.
XX
XX 30-MAY-1996; 96WO-US08014.
XX
XX 20-MAR-1996; 96US-0618693.
XX 02-JUN-1995; 95US-0458423.
XX 02-JUN-1995; 95US-0458424.
XX 05-JUN-1995; 95US-0465591.
XX 05-JUN-1995; 95US-0465594.
XX 07-JUN-1995; 95US-0479725.
XX 07-JUN-1995; 95US-0479783.
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Janjic N, Pagratia N, Ringquist S, Toothman PJ;
XX WPI; 1997-034387/03.
XX
XX Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF -
PT using SELEX, used in the diagnosis and treatment of proliferative
PT disorders
XX
XX Claim 39; Page 140; 209pp; English.
XX
XX The present sequence, a platelet derived growth factor (PDGF)
CC binding ligand, was identified by Systematic Evolution of Ligands
CC by Exponential enrichment (SELEX). Briefly a candidate mixture of
CC nucleic acids was contacted with PDGF, and nucleic acids having an
CC increased affinity to PDGF partitioned from the remainder of the
CC mixture. The partitioned nucleic acids were then amplified to yield
CC a mixture of nucleic acids enriched for sequences with higher

CC affinity and specificity for binding to PDGF. The ligand is
CC anti-mitogenic and may be used to inhibit epithelial cell
CC proliferation, or in the diagnosis and treatment of PDGF mediated
CC pathological conditions, e.g. to inhibit the development of
CC neointimal lesions following arterial injury.

XX Sequence 96 BP; 25 A; 23 C; 29 G; 18 U; 1 other;
SQ
Query Match 1.2%; Score 23.2; DB 18; Length 96;
Best Local Similarity 44.7%; Pred. No. 2.5e+04;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;
QY 737 ATGAATAAGACCAACATACACATGTCATATGATGAATAAGTTCTGGGGATAAAGCAT 796
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8 AAGAUAUACGCUAACCCUGGUGGNGGGAAGUAGUACUAGUUGGCGCUACUCAU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAAC 821
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
68 UCGCCUUCGACAGGAGGCUACAC 92

RESULT 41
AAx87067
ID AAX87067 standard; RNA; 96 BP.
XX
AC AAX87067;
XX
DT 20-SEP-1999 (first entry)
XX
DE Platelet derived growth factor RNA ligand.
XX
KW Platelet derived growth factor; PDGF; human; ligand; SELEX;
KW systematic evolution of ligands by exponential enrichment;
KW angiogenesis; restenosis; tumour; cancer; fibrosis; therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..96 /*tag= a
FT /mod_base= OTHER
FT /note= "all pyrimidines are 2'-F modified"

XX WO9931119-A1.
XX
XX 24-JUN-1999.
XX
XX 29-APR-1998; 98WO-US09050.
XX
XX 16-DEC-1997; 97US-0991743.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Janjic N;
XX
XX WPI; 1999-405022/34.
XX
XX Complex comprises a platelet derived growth factor nucleic acid
PT ligand

XX Example 10; Page 91; 156pp; English.
XX
XX This sequence represents a 2'-fluoropyrimidine RNA high affinity
CC ligand to human platelet derived growth factor (PDGF). It is one
CC of 43 high affinity RNA ligands (see AAX87039-81) to PDGF-AB that
CC were identified in a SELEX (systematic evolution of ligands by
CC exponential enrichment) process from a library of RNA molecules
CC (see AAX87036). The invention discloses a method for preparing a
CC complex of a PDGF nucleic acid ligand and a non-immunogenic high
CC mol.wt. compound (e.g. PEG) or lipophilic compound (e.g. a glycerol
CC lipid). Such complexes are used as inhibitors of PDGF mediated
CC angiogenesis, to inhibit the growth of tumours, to inhibit fibrosis
CC (especially kidney, lung, bone marrow or radiation treatment

CC associated fibrosis) or to inhibit restenosis, especially in-stent
CC restenosis or restenosis in a coronary artery or non-coronary
CC vessel. They can also be used to target a therapeutic or
CC diagnostic agent to a biological target expressing PDGF.

XX Sequence 96 BP; 25 A; 23 C; 29 G; 18 U; 1 other;
SQ
Query Match 1.2%; Score 23.2; DB 20; Length 96;
Best Local Similarity 44.7%; Pred. No. 2.5e+04;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;
QY 737 ATGAATAAGACCAACATACACATGTCATATGATGAATAAGTTCTGGGGATAAAGCAT 796
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8 AAGAUAUACGCUAACCCUGGUGGNGGGAAGUAGUACUAGUUGGCGCUACUCAU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAAC 821
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
68 UCGCCUUCGACAGGAGGCUACAC 92

RESULT 42
AAx92339/c
ID AAT92339 standard; RNA; 76 BP.
XX
AC AAT92339;
XX
DT 26-JAN-1998 (first entry)
XX
DE Ribozyme (15) to specifically cleave HIV RNA.
XX
KW Ribozyme; HIV; human immunodeficiency disease; AIDS; tumour;
KW tRNA anti-codon stem loop; hairpin loop; target; substrate; ss.
XX
OS Synthetic.
OS Human immunodeficiency virus type 1.
XX
FH Key Location/Qualifiers
FT stem_loop 1..43 /*tag= a
XX
XX JP09220094-A.
XX
XX 26-AUG-1997.
XX
XX 12-DEC-1996; 96JP-0331843.
XX
XX 13-DEC-1995; 95JP-0324778.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI; 1997-474308/44.
XX
XX Ribozyme having a tRNA anti-codon stem loop - used to specifically
PT cleave a natural polynucleotide or RNA that is detrimental to the
PT living body
XX
XX Example 5; Page 30; 33pp; Japanese.

XX The present sequence represents a polynucleotide with ribozyme
CC activity which contains a tRNA anti-codon stem loop. By administering
CC a vector containing the DNA encoding the ribozyme into the living body,
CC its product (a ribozyme) can specifically cleave a natural
CC polynucleotide or RNA detrimental to the living body, and so it can
CC be used preventatively and therapeutically against AIDS and various
CC tumours caused by RNA. The present sequence acts against HIV RNA.

XX Sequence 76 BP; 40 A; 13 C; 11 G; 12 U; 0 other;
SQ
Query Match 1.2%; Score 23; DB 18; Length 76;
Best Local Similarity 63.6%; Pred. No. 2.6e+04;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 828 CTGTTTCTGGAAGTGTCTTTCTTTAGGTTGCTCTCGGTTTGAGCGCTG 882

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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 05:46:43 ; Search time 132 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 830080

Minimum DB seq length: 5
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24.4	1.3	95	4	US-09-087-609-13
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3	24	1.3	78	2	US-08-398-615-22
4	24	1.3	78	3	US-08-397-303-22
5	23.2	1.2	96	1	US-08-479-783A-67
6	23.2	1.2	96	1	US-08-479-725-67
7	23.2	1.2	96	1	US-08-618-693-67
8	23.2	1.2	96	3	US-08-373-124-156
9	23.2	1.2	96	3	US-08-991-743C-67
10	23.2	1.2	96	4	US-09-851-486-67
11	23.2	1.2	96	5	PCT-US96-08014-156
12	22.8	1.2	85	3	US-08-321-887-36
13	22.8	1.2	100	1	US-08-145-705A-29
14	22.6	1.2	69	3	US-08-584-760A-34
15	22.6	1.2	91	4	US-09-328-750A-5
16	22.6	1.2	96	1	US-08-479-783A-61
17	22.6	1.2	96	1	US-08-479-725-61
18	22.6	1.2	96	1	US-08-618-693-61
19	22.6	1.2	96	3	US-08-973-124-150
20	22.6	1.2	96	3	US-08-991-743C-61
21	22.6	1.2	96	4	US-09-851-486-61
22	22.6	1.2	96	5	PCT-US96-08014-150
23	22.6	1.2	100	1	US-08-472-255A-15
24	22.6	1.2	100	1	US-08-479-724A-15
25	22.6	1.2	100	3	US-08-472-256B-15
26	22.6	1.2	100	3	US-08-952-793-15
27	22.6	1.2	100	4	US-09-849-928-15

c	28	22.6	1.2	100	5	PCT-US96-09455A-15	Sequence 15, Appl
	29	22.4	1.2	72	1	US-08-303-275-195	Sequence 195, App
	30	22.4	1.2	90	3	US-08-974-549A-675	Sequence 675, App
c	31	22.4	1.2	90	3	US-08-974-549A-676	Sequence 676, App
	32	22.2	1.2	47	4	US-09-422-978-1231	Sequence 1231, App
c	33	22.2	1.2	84	6	5217864-2	Patent No. 5217864
c	34	22.2	1.2	96	1	US-08-253-877C-16	Sequence 16, Appl
c	35	22.2	1.2	96	2	US-08-452-164A-16	Sequence 16, Appl
c	36	22.2	1.2	96	3	US-08-603-024-15	Sequence 15, Appl
c	37	22.2	1.2	96	4	US-08-450-809-11	Sequence 11, Appl
c	38	22.2	1.2	97	1	US-08-145-939-7	Sequence 7, Appl
c	39	22.2	1.2	97	1	US-08-343-267-7	Sequence 7, Appl
	40	22	1.2	91	3	US-09-084-120-23	Sequence 23, Appl
	41	21.8	1.2	80	4	US-09-308-759A-18	Sequence 18, Appl
c	42	21.8	1.2	87	3	US-09-237-712-3	Sequence 3, Appl
c	43	21.8	1.2	87	4	US-09-394-457C-13	Sequence 13, Appl
c	44	21.8	1.2	87	4	US-09-709-586A-13	Sequence 13, Appl
c	45	21.8	1.2	87	4	US-09-655-104A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-087-609-13
; Sequence 13, Application US/09087609
; Patent No. 6537972
; GENERAL INFORMATION:
; APPLICANT: Holzmayer, Tanya A.
; APPLICANT: Dunn, Stephen J.
; APPLICANT: Dayn, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: INHIBITING HUMAN IMMUNODEFICIENCY VIRUS INFECTION BY
; TITLE OF INVENTION: DOWN-REGULATING HUMAN CELLULAR GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,609
; FILING DATE: May 29, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 9320-0009-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-087-609-13

Query Match 1.3%; Score 24.4; DB 4; Length 95;
Best Local Similarity 58.1%; Pred. No. 1.6e+03;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: P889
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-397-303-22

Query Match 1.3%; Score 24; DB 3; Length 78;
Best Local Similarity 64.3%; Pred. No. 1.9e+03;
Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1659 TTATTATGACCATAGGATCTCTTAGGAACCTTATCGCTCTTTATATTGCACCA 1714
DB 11 TCAAAAAGAACATAGCGTTCTCTTGCACTCATGTTCGTTTTTCTATTGCTACA 66

RESULT 5
US-08-479-783A-67
Sequence 67, Application US/08479783A
Patent No. 5668264
GENERAL INFORMATION:
APPLICANT: NEBOUSA JANJIC
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
TITLE OF INVENTION: ACID LIGANDS
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,783A
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX42-2
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:

LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F
OTHER INFORMATION: modified
US-08-479-783A-67

Query Match 1.2%; Score 23.2; DB 1; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.5e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;
QY 737 ATGAATAAGACCCCAATACACAGTTGCATGATGATGAATAAGTTCGTGGGATAAAGCAT 796
DB 8 AAGAUAACGCUCAACCCUGGUGGNGGGRAGUUAUCAGUUGGCGCUCUACUCAU 67
QY 737 GATTTCCTTGAGAGGATGCAAAAAC 821
DB 68 UCGCCUUCGACAGGAGGCUCAAC 92

RESULT 6
US-08-479-725-67
Sequence 67, Application US/08479725
Patent No. 5674685
GENERAL INFORMATION:
APPLICANT: NEBOUSA JANJIC
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
TITLE OF INVENTION: ACID LIGANDS
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,725
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX42-1
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:

```
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F
; OTHER INFORMATION: modified
US-08-479-725-67

Query Match      1.2%; Score 23.2; DB 1; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.5e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGAATAAGACCCAAACATACACAGTTCATATGATGAATAGTTCGTTGGGATAAGCAT 796
Db 8 AAGAAUAACCGCAACCGGAGGNGGGAAGUUAUCAGUUGGCGCUCACUCAU 67

QY 797 GATTTCCTTGAGAGGATGCAAAAAAC 821
Db 68 UCGCCUUCGACAGAGGCGUCACAC 92

RESULT 7
US-08-618-693-67
; Sequence 67, Application US/08618693
; Patent No. 5723594
; GENERAL INFORMATION:
; APPLICANT: NEBOJSA JANJIC
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,693
; FILING DATE: 20 MARCH 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 7-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX42/CIP
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F
; OTHER INFORMATION: modified
US-08-618-693-67

Query Match      1.2%; Score 23.2; DB 1; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.5e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGAATAAGACCCAAACATACACAGTTCATATGATGAATAGTTCGTTGGGATAAGCAT 796
Db 8 AAGAAUAACCGCAACCGGAGGNGGGAAGUUAUCAGUUGGCGCUCACUCAU 67

QY 797 GATTTCCTTGAGAGGATGCAAAAAAC 821
Db 68 UCGCCUUCGACAGAGGCGUCACAC 92

RESULT 8
US-08-973-124-156
; Sequence 156, Application US/08973124
; Patent No. 6207816
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD et al.
; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
; TITLE OF INVENTION: LIGANDS TO GROWTH
; TITLE OF INVENTION: FACTORS
; NUMBER OF SEQUENCES: 304
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,124
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08014
; FILING DATE: 30-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,423
; FILING DATE: 02-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,424
; FILING DATE: 02-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,594
; FILING DATE: 05-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,591
; FILING DATE: 05-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,725
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/618,693
; FILING DATE: 20-MARCH-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F modified
US-08-973-124-156

Query Match 1.2%; Score 23.2; DB 3; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.5e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGAATAAGACCCACATACACAGTTCATATGATGAATAAGTTCGTGGGATAAGCAT 796
DB 8 AAGAAUACGCUCAACCGUAGGNGGGAAGUUAUCAGUUGGCGCUCUACU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAC 821
DB 68 UCGCCUUCGACAGGAGGCUCAAC 92

RESULT 9

US-08-991-743C-67
Sequence 67, Application US/08991743C
Patent No. 6229002
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANJIC, LARRY GOLD
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
ACID LIGAND COMPLEXES

NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado
COUNTRY: USA
ZIP: 80129

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,743C
FILING DATE: 16-Dec-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
APPLICATION NUMBER: 08/479,783
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/479,725
FILING DATE: 7-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 268-0066
TELEFAX: (303) 268-0065

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA

FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F modified
SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Query Match 1.2%; Score 23.2; DB 3; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.5e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

US-08-991-743C-67

QY 737 ATGAATAAGACCCACATACACAGTTCATATGATGAATAAGTTCGTGGGATAAGCAT 796
DB 8 AAGAAUACGCUCAACCGUAGGNGGGAAGUUAUCAGUUGGCGCUCUACU 67
QY 797 GATTTCTTGAGAGGATGCAAAAAC 821
DB 68 UCGCCUUCGACAGGAGGCUCAAC 92

RESULT 10

US-09-851-486-67
Sequence 67, Application US/09851486
Patent No. 6582918
GENERAL INFORMATION:

APPLICANT: NEBOJSA JANJIC, LARRY GOLD
TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
ACID LIGAND COMPLEXES

NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,486
FILING DATE: 08-May-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/991,743
FILING DATE: 16-DECEMBER-1997
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
APPLICATION NUMBER: 08/479,783
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/479,725
FILING DATE: 7-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA

FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F modified
SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Query Match 1.2%; Score 23.2; DB 4; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.5e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGAATAAGACCCACATACACAGTTCATATGATGAATAAGTTCGTGGGATAAGCAT 796
DB 8 AAGAAUACGCUCAACCGUAGGNGGGAAGUUAUCAGUUGGCGCUCUACU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAC 821
DB 68 UCGCCUUCGACAGGAGGCUCAAC 92

PCT-US96-08014-156

SEQUENCE INFORMATION:
 ; APPLICANT: LARRY GOLD; NBOJSA JANJIC; STEVEN RINGQUIST;
 ; APPLICANT: PAGRATIS; PENELOPE J. TOOTHMAN
 ; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
 ; TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
 ; TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED
 ; TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
 ; TITLE OF INVENTION: KEROTINOCYTE GROWTH FACTOR (hKGF)
 ; NUMBER OF SEQUENCES: 304
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WordPerfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/08014
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/458,423
 ; FILING DATE: 02-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/458,424
 ; FILING DATE: 02-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/465,594
 ; FILING DATE: 05-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/465,591
 ; FILING DATE: 05-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/479,725
 ; FILING DATE: 07-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/479,783
 ; FILING DATE: 07-JUNE-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/618,693
 ; FILING DATE: 20-MARCH-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barry J. Swanson
 ; REGISTRATION NUMBER: 33,215
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 793-3333
 ; TELEFAX: (303) 793-3433
 ; INFORMATION FOR SEQ ID NO: 156:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 96 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA
 ; FEATURE:
 ; OTHER INFORMATION: All pyrimidines are 2'-F modified

PCT-US96-08014-156

Query Match 1.2%; Score 23.2; DB 5; Length 96;
 Best Local Similarity 44.7%; Pred. No. 3.5e+03;
 Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;
 QY 737 ATGAATAAGACCAACATACACAGTTCATATGATGAATAAGTTCGTGGGATAAAGCAT 796

RESULT 11

US-08-921-887-36
 ; Sequence 36, Application US/08921887
 ; Patent No. 6030771
 ; GENERAL INFORMATION:
 ; APPLICANT: KHUYAKOV, YURI E.
 ; APPLICANT: FIELDS, HOWARD A.
 ; TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
 ; TITLE OF INVENTION: ENDONUCLEASE ASSISTED LIGATION METHOD FOR MAKING THE SAME
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: JONES & ASKEW, LLP
 ; STREET: 191 Peachtree Street, N.W., 37th Floor
 ; CITY: Atlanta
 ; STATE: GA
 ; COUNTRY: USA
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/921,887
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARREN, WILLIAM L.
 ; REGISTRATION NUMBER: 36,714
 ; REFERENCE/DOCKET NUMBER: 03063-0380
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-818-3700
 ; TELEFAX: 404-818-3799
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 85 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Hepatitis virus
 ; US-08-921-887-36

US-08-921-887-36

Query Match 1.2%; Score 22.8; DB 3; Length 85;
 Best Local Similarity 62.1%; Pred. No. 4.2e+03;
 Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
 QY 868 CGGGTTTGGAGCTCGAATTCGGTTTGGGAATGGATTTTAAAGGAGGGTATGCCTTT 925
 Db 26 CGTATATCGAGCAGGGAATGCTAGCTAGTGAACAGTTTAAACAGAGGCTCTGGCTTT 83

RESULT 13

US-08-145-705A-29/c
 ; Sequence 29, Application US/08145705A
 ; Patent No. 5489513
 ; GENERAL INFORMATION:
 ; APPLICANT: Springer, Wolfgang; Plempel, Manfred;
 ; APPLICANT: L bberding, Antonius
 ; TITLE OF INVENTION: SPECIFIC GENE PROBES AND
 ; TITLE OF INVENTION: PROCESSES FOR THE DIAGNOSTIC

;; TITLE OF INVENTION: INVESTIGATION OF CANDIDA
;; TITLE OF INVENTION: ALBICANS
;; NUMBER OF SEQUENCES: 44
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
;; STREET: 660 White Plains Road
;; CITY: Tarrytown
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10591-5144
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
;; COMPUTER: NEC PowerMate 1 Plus
;; OPERATING SYSTEM: DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/145,705A
;; FILING DATE: October 28, 1993
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: German P 42 36 708.5
;; FILING DATE: October 30, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kurt G. Briscoe
;; REGISTRATION NUMBER: 33,141
;; REFERENCE/DOCKET NUMBER: Bayer 8885-KGB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (914) 332-1700
;; TELEFAX: (914) 332-1844
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 100 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Candida albicans
US-08-145-705A-29

Query Match 1.2%; Score 22.8; DB 1; Length 100;
Best Local Similarity 62.1%; Pred. No. 4.6e+03;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1347 CTTTAAATTCATGACCTTTGGTACCTGTGACGTCTTGTATAGCACATTTCTTTT 1404
Db 58 CTTTATTTCTGCATATTTATCATCATCTGCATTATTTATATCAAGGCTGTTTT 1

RESULT 14
US-08-584-760A-34/c
; Sequence 34, Application US/08584760A
; Patent No. 6290953
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J
; APPLICANT: Courtney, Michael G
; APPLICANT: Finnis, Christopher J A
; APPLICANT: Sleep, Darrell
; TITLE OF INVENTION: Medicine
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centeon L.L.C.
; STREET: 1020 First Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,760A
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/211,860
;; FILING DATE: 15-APR-1994
;; APPLICATION NUMBER: GB 9121815.6
;; FILING DATE: 14-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Naomi Biswas
;; REGISTRATION NUMBER: 38,384
;; REFERENCE/DOCKET NUMBER: 92H853-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610/878-4294
;; TELEFAX: 610/878/4221
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 69 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..69
;; OTHER INFORMATION: /function= "oligonucleotide 33"
US-08-584-760A-34
Query Match 1.2%; Score 22.6; DB 3; Length 69;
Best Local Similarity 58.0%; Pred. No. 4.4e+03;
Matches 40; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 951 TCAGCGATGTTGCTCAATGCGTGCAAAAGTTGTGCATAAACTACAGGAAGCTGGTCTTT 1010
Db 69 TCACGTGATATGCTAGATTAGTGATCAAGTTGATGGTCAAGACCATTAGCTGTATTC 10
QY 1011 CTTCTAGAG 1019
Db 9 ATGCTAAAG 1
RESULT 15
US-09-328-750A-5/c
; Sequence 5, Application US/09328750A
; Patent No. 6410722
; GENERAL INFORMATION:
; APPLICANT: McGill University et al.
; TITLE OF INVENTION: REPLICATION ORIGIN CONSENSUS SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SWABEY OGILVY RENAULT
; STREET: 1981 McGill College Avenue - Suite 1600
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,750A
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,374

```

; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: 60/047,322
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: C't., France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-163PCT FC/ld
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514 288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-328-750A-5

```

```

Query Match      1.28; Score 22.6; DB 4; Length 91;
Best Local Similarity 13.6%; Pred. No. 5e+03;
Matches 11; Conservative 41; Mismatches 23; Indels 0; Gaps 0;

Qy 1591 AGCTACAACCTCATCAGTTTGGTAAATGCTTTGTTTATAGGGGGCTCCCTCTGCTTTAA 1650
Db 90 ATYKQMMHTMMWMMMTATHSMTWMMWKYCMRYRTWAWCCMWAMTMTMHHKGTSTYDW 31

Qy 1651 TTTTGCATTATTATGACCATT 1671
Db 30 BMWMMWYNTICWBTHMMWMMWYWT 10

```

RESULT 16
US-08-479-783A-61
; Sequence 61, Application US/08479783A
; Patent No. 5668264
; GENERAL INFORMATION:
; APPLICANT: NEBOJSA JANIIC
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C. #200
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,783A
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:

```

: APPLICATION NUMBER: 07/536,428
: FILING DATE: 11-JUNE-1990
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Diane H. McClearn
: REGISTRATION NUMBER: 33,960
: REFERENCE/DOCKET NUMBER: NEX42-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 61:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 96 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA
: FEATURE:
: OTHER INFORMATION: All pyrimidines are 2'-F
: OTHER INFORMATION: modified
:
: US-08-479-783A-61
:
: Query Match 1.2%; Score 22.6; DB 1; Length 96;
: Best Local Similarity 44.7%; Pred. No. 5.1e+03;
: Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;
:
: Qy 737 ATGAATTAAGACCAACATACACAGTGTGCATATGATGAATAGTTCTGTGGGATAAAGCAT 796
:
: Db 8 AAGAAUAAACCCUACACUGAGUGGGGGGAAGUUGAUAUCAGUUGCGGCUCUACU 67
:
: Qy 797 GATTTCTTGTGAGAGTCAAAAAAC 821
:
: Db 68 UCGCCUUCGACAGGAGGCUCACACAC 92

```

RESULT 17
US-08-479-725-61
; Sequence 61, Application US/08479725
; Patent No. 5674685
; GENERAL INFORMATION:
; APPLICANT: NEROJSA JANJIC
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,725
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F
; OTHER INFORMATION: modified
US-08-618-693-61

Query Match 1.2%; Score 22.6; DB 1; Length 96;
Best Local Similarity 44.7%; Pred. NO. 5.1e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGATAAGACCCACATACACAGTTCATATGATGAATAAGTCTGGGATAAAGCAT 796
Db 8 AAGAAUAAAGCCUACACCGUAGUGGGGGAAGAUUAGUUGUGGCGCUCACUCAU 67
QY 797 GATTTCTTCGAGAGGATGCAAAAAC 821
Db 68 UGCGCUUCCAGACAGGAGGCUCACAAAC 92

RESULT 19
US-08-973-124-150
; Sequence 150, Application US/08973124
; Patent No. 6207816
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD et al.
; TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
; TITLE OF INVENTION: LIGANDS TO GROWTH
; TITLE OF INVENTION: FACTORS
; NUMBER OF SEQUENCES: 304
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,124
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08014
; FILING DATE: 30-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,423
; FILING DATE: 02-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,424
; FILING DATE: 02-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,594
; FILING DATE: 05-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,591
; FILING DATE: 05-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,725
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/618,693
; FILING DATE: 20-MARCH-1996
; ATTORNEY/AGENT INFORMATION:

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F modified
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-08-991-743C-61

Query Match      1.2%; Score 22.6; DB 3; Length 96;
Best Local Similarity 44.7%; Pred. No. 5.1e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGATAAGACCCACATACACAGTTGCATATGATGAATTAAGTTCTGTTGGGATAAAGCAT 796
DB   |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
      8 AAGAUAUACGCUAACCCUGAGUGGGGGAAGUUAUAGUUGGCGCUCUACUACAU 67

QY 797 GATTTCCTTGAGAGGATGCAAAAAC 821
DB   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
      68 UGCUUUCGACAGGAGGCUACACAC 92

RESULT 21
US-09-851-486-61
; Sequence 61, Application US/09851486
; Patent No. 6582918
; GENERAL INFORMATION:
; APPLICANT: NEBOJSA JANJIC, LARRY GOLD
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
; ACID LIGAND COMPLEXES
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,486
; FILING DATE: 08-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 16-DECEMBER-1997
; APPLICATION NUMBER: 08/618,693
; FILING DATE: 20-MARCH-1996
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/479,725
; FILING DATE: 7-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX66
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F modified
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-851-486-61

Query Match      1.2%; Score 22.6; DB 4; Length 96;

```


Best Local Similarity 44.7%; Pred. No. 5.1e+03; Mismatches 38; Conservative 8; Indels 0; Gaps 0;

QY 737 ATGAATAAGACCAACATACACAGTTGCATATGATCAATAAGTTCTGTGGGATAAAGCAT 796
Db 8 AGAUAUACGCCUACACCUAGUAGGGGGAAGUUAUCAGUUGGCGCUCACUACAU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAC 821
Db 68 UGCGCUUCGACAGGAGGCUACAAC 92

RESULT 22
PCT-US96-08014-150
Sequence 150, Application PC/TUS9608014
GENERAL INFORMATION:
APPLICANT: LARRY GOLD; NEBOJSA JANJIC; STEVEN RINGQUIST; NIKOS
APPLICANT: PAGRATIS; PENELOPE J. TOOTHMAN
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
TITLE OF INVENTION: KEROTINOCYTE GROWTH FACTOR (hKGF)
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 150:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-F modified
PCT-US96-08014-150

Query Match 1.2%; Score 22.6; DB 5; Length 96;
Best Local Similarity 44.7%; Pred. No. 5.1e+03;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGAATAAGACCAACATACACAGTTGCATATGATCAATAAGTTCTGTGGGATAAAGCAT 796
Db 8 AAGAUAUACGCCUACACCUAGUAGGGGGAAGUUAUCAGUUGGCGCUCACUACAU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAC 821
Db 68 UGCGCUUCGACAGGAGGCUACAAC 92

RESULT 23
US-08-472-255A-15/c
Sequence 15, Application US/08472255A
Patent No. 5766853
GENERAL INFORMATION:
APPLICANT: PARMA, DAVID
APPLICANT: GOLD, LARRY
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: TO SELECTINS (AS AMENDED)
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,255A
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-472-255A-15


```

: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 6.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/09/849,928
: FILING DATE: 04-May-2001
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/952,793
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/479,724
: FILING DATE: 07-JUNE-1995
: APPLICATION NUMBER: 08/472,256
: FILING DATE: 07-JUNE-1995
: APPLICATION NUMBER: 08/472,255
: FILING DATE: 07-JUNE-1995
: APPLICATION NUMBER: 08/477,829
: FILING DATE: 07-JUNE-1995
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEX40C/PCT
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 100 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: RNA
: FEATURE:
:
: OTHER INFORMATION: All C's are 2'-NH2 cytosine
:
: OTHER INFORMATION: All U's are 2'-NH2 uracil
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 15:
:
: US-09-849-928-15
:
: Query Match 1.2%; Score 22.6; DB 4; Length 100
: Best Local Similarity 68.9%; Pred. No. 5.2e+03;
: Matches 31; Conservative 0; Mismatches 14; Indels
:
: Qy 1345 CGCTTTAATTCATGCACCTTTTGGCTACCTGTGCAGCTCTTGTTAT 1349
: | | | | |
: Db 59 CGTTC TAATTCAGTACACTTTCGATTCGCCGCCGAGTCCTTGAT 15
: | | | | |
:
: RESULT 28
: PCT-US96-09455A-15/c
: Sequence 15. Application PC/TUS9609455A
:
: GENERAL INFORMATION:
: APPLICANT: PARMA, et al.
: TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
: TITLE OF INVENTION: LIGANDS TO LECTINS
: NUMBER OF SEQUENCES: 390
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
: COMPUTER: IBM pc compatible
: OPERATING SYSTEM: MS-DOS

```



```

; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 675:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..90
; OTHER INFORMATION: /note= "oligonucleotide 178"
; US-08-974-549A-675

```

```

Query Match 1.2%; Score 22.4; DB 3; Length 90;
Best Local Similarity 56.9%; Pred. NO. 5.6e+03;
Matches 41; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1517 AACCTGTTTACCCCTATGATGTTTGTAGTTAATGATGCCCTTCAAAAGACGTTTCAGCCGC 1576
Db 11 ACGGTGTTTACCCAGGAGATGAATTTTGTGTTACCGAGAAACGACGTTCTGTGTG 70

QY 1577 ACGGTAATGACA 1588
Db 71 ACGGGAACCCCA 82

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RESULT 31
US-08-974-549A-676/c
; Sequence 676, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/974,549A
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 676:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..90
; OTHER INFORMATION: /note= "oligonucleotide 177"
; US-08-974-549A-676

```

```

Query Match 1.2%; Score 22.4; DB 3; Length 90;
Best Local Similarity 56.9%; Pred. NO. 5.6e+03;
Matches 41; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1517 AACCTGTTTACCCCTATGATGTTTGTAGTTAATGATGCCCTTCAAAAGACGTTTCAGCCGC 1576
Db 90 ACGGTGTTTACCCAGGAGATGAATTTTGTGTTACCGAGAAACGACGTTCTGTGTG 31

QY 1577 ACGGTAATGACA 1588
Db 30 ACGGGAACCCCA 19

RESULT 32

```

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US-09-422-978-1231
; Sequence 1231, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1231
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-22167-79 : polymorphic base C or T
US-09-422-978-1231

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```

Query Match 1.2%; Score 22.2; DB 4; Length 47;
Best Local Similarity 69.8%; Pred. No. 4.8e+03;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 691 AATGTTACGGCTTTTCATGACTAAATTTTCTTCATCTG 733
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 AAAATTAGATCTCTTCCVTAATAAATTAGGCTTCATCTG 47

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RESULT 33
5217864-2/c
; Patent No. 5217864
; APPLICANT: HEINTZ, NATHANIEL; DAILEY, LISA A.; HEINTZ,
; NICHOLAS H.; CADDE, MARK S.
; TITLE OF INVENTION: REPLICATION INITIATOR PROTEIN COMPLEX
; AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/573,570
; FILING DATE: 27-AUG-1990
; SEQ ID NO:2:
; LENGTH: 84
5217864-2

```

```

Query Match 1.2%; Score 22.2; DB 6; Length 84;
Best Local Similarity 58.2%; Pred. No. 6.1e+03;
Matches 39; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 519 TTTTATGCTCAAGCTTAAATAATCTGATAAAGATATACCAAGGCTTTGGAG 578
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 TTTTGTGCAAACTCAGTAAAGAACTAATAATAAATAAATAAATAAATAAATAA 8

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QY 579 CCATTTT 585
|||||
Db 7 TCATTTT 1

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RESULT 34
US-08-253-877C-16/c
; Sequence 16, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hamann, Lois
; APPLICANT: Hollander, Irwin

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; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-253-877C-16

Query Match 1.2%; Score 22.2; DB 1; Length 96;
Best Local Similarity 77.1%; Pred. No. 6.5e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 407 CTACAGTATTTGGATGCGCCACTCACCTTGTCAGG 441
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 CTACATTATTTGGATGAGACAGGACCTGGACAGG 39

RESULT 35
US-08-452-164A-16/c
; Sequence 16, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hamann, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-452-164A-16

Query Match 1.2%; Score 22.2; DB 2; Length 96;
Best Local Similarity 77.1%; Pred. No. 6.5e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 407 CTACAGTATTGGATCGGCCACTCACCTTGTTCAGG 441
|||||
DB 73 CTACATTATTGGATGAGACAGGCACCTGGACAGG 39

RESULT 36
US-08-603-024-15/c
; Sequence 15, Application US/08603024
; Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Hinman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hamann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-603-024-15

Query Match 1.2%; Score 22.2; DB 3; Length 96;
Best Local Similarity 77.1%; Pred. No. 6.5e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 407 CTACAGTATTGGATCGGCCACTCACCTTGTTCAGG 441
|||||
DB 73 CTACATTATTGGATGAGACAGGCACCTGGACAGG 39

RESULT 37
US-08-450-809-11/c
; Sequence 11, Application US/08450809
; Patent No. 6506881
; GENERAL INFORMATION:
; APPLICANT: Adair et al.
; TITLE OF INVENTION: Anti-HMFG Antibodies and
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6506881ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,809
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/948,541B
; FILING DATE: 9/22/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Joanne Longo Feeney
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: CELL-0004
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-450-809-11

Query Match 1.2%; Score 22.2; DB 4; Length 96;
Best Local Similarity 77.1%; Pred. No. 6.5e+03;
Matches 27; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 407 CTACAGTATTGGATCGGCCACTCACCTTGTTCAGG 441
|||||
DB 73 CTACATTATTGGATGAGACAGGCACCTGGACAGG 39

RESULT 38
US-08-145-939-7/c
; Sequence 7, Application US/08145939
; Patent No. 5554501
; GENERAL INFORMATION:
; APPLICANT: Coassin, Peter J.
; APPLICANT: Matson, Robert
; APPLICANT: Rampal, Jang
; TITLE OF INVENTION: BIOPOLYMER SYNTHESIS USING SURFACE
; MOLECULE TYPE: ACTIVATED, ORGANIC POLYMERS
; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Robbins, Berliner & Carson
; STREET: 201 No. 554501th Figueroa Street, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,939
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 5727-109C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-145-939-7

Query Match 1.2%; Score 22.2; DB 1; Length 97;
Best Local Similarity 54.2%; Pred. No. 6.5e+03;
Matches 45; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 572 TTGGAGCCATTTTGATCTTAAGG 654
|||||
Db 88 TTGTGACGCTTCTGTATCTATTCATCATAGGAACCAAGATGATATTTCTTT 29
|||||

QY 632 CTAGATACAGGCGCTATTAAAGG 654
|||||
Db 28 AATGGTCCAGGCATATCCAGG 6
|||||

RESULT 39
US-08-343-267-7/c
; Sequence 7, Application US/08343267
; Patent No. 5583211
; GENERAL INFORMATION:
; APPLICANT: Coassin, Peter J.
; APPLICANT: Matson, Robert S.
; APPLICANT: Rampal, Jang B.
; TITLE OF INVENTION: Biopolymer Synthesis
; TITLE OF INVENTION: Utilizing Surface
; TITLE OF INVENTION: Activated, Organic
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44
; MEDIUM TYPE: Mb
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,267
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,100
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Burgoon, Richard P.
; REGISTRATION NUMBER: 34,787
; REFERENCE/DOCKET NUMBER: 129D-141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-6969
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-343-267-7

Query Match 1.2%; Score 22.2; DB 1; Length 97;
Best Local Similarity 54.2%; Pred. No. 6.5e+03;
Matches 45; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 572 TTGGAGCCATTTTGATCTTAAGG 654
|||||
Db 88 TTGTGACGCTTCTGTATCTATTCATCATAGGAACCAAGATGATATTTCTTT 29
|||||

QY 632 CTAGATACAGGCGCTATTAAAGG 654
|||||
Db 28 AATGGTCCAGGCATATCCAGG 6
|||||

RESULT 40
US-09-084-120-23
; Sequence 23, Application US/09084120
; Patent No. 6251592
; GENERAL INFORMATION:
; APPLICANT: TANG, JianQing
; APPLICANT: MELANCON, Serge B.
; TITLE OF INVENTION: A NOVEL STR MARKER SYSTEM
; TITLE OF INVENTION: FOR DNA FINGERPRINTING
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SWABEY OGILVY RENAULT
; STREET: Suite 1600, 1981 McGill College Avenue
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,120
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: COTE, France
; REGISTRATION NUMBER: 37,037
; REFERENCE/DOCKET NUMBER: 13251-4US FC/ld
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126


```
; TELEFAX: 514 288-8389
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-084-120-23

Query Match          1.2%; Score 22; DB 3; Length 91;
Best Local Similarity 59.7%; Pred. No. 7.2e+03;
Matches 37; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1103 CGAGCCTCTCTCTAAATAACGATCATGAGCTGGCGTTATTGTGGGATTGTGTGAGA 1162
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6 CGAGACTCTGTCATAATAAACAACAACAACAACTCTGGTTCTCTGGCGCTTCTCTTGAAA 65

QY 1163 AA 1164
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
66 TA 67

RESULT 41
US-09-308-759A-18
; Sequence 18, Application US/09308759A
; Patent No. 6391593
; GENERAL INFORMATION:
; APPLICANT: Weston, Anthony
; Assenberg, Rene
; Marsh, Peter
; Mock, Graham A.
; Ray, Trevor D.
; Wharam, Susan D.
; Cardy, Donald L.N.
; TITLE OF INVENTION: Modified Nucleic Acid Probes and Uses Thereof
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: PILLSBURY WINTHROP LLP
; STREET: 1600 TYSONS BOULEVARD
; CITY: McLean
; STATE: VA
; COUNTRY: USA
; ZIP: 22102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,759A
; FILING DATE: 19-Jul-1999
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-308-759A-18

Query Match          1.2%; Score 21.8; DB 4; Length 80;
Best Local Similarity 65.3%; Pred. No. 7.7e+03;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 809 GGATGCAAAAACCTTGGCGCTGTTCTTGGAGTGTTTTTCTTTTAGGTT 857
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
32 GAATGCAAAACACTGACTGAGAAGTTCTTGAGAAATGCTTCTGTTGATTTT 80

RESULT 42
US-09-237-712-3/c

Query Match          1.2%; Score 21.8; DB 3; Length 87;
Best Local Similarity 61.4%; Pred. No. 8e+03;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1652 TTTCATTTTATTATGACCATAGGATTTCTTCTAGGAACCTTTATCGTCTTTATATT 1708
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 TTATTCTTATTATAACCATATGGATTATTAAAGCAAGCTTCTTTTCGTTTGCTTT 25

RESULT 43
US-09-394-457C-13/c
; Sequence 13, Application US/09394457C
; Patent No. 6440705
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 246/020
; CURRENT APPLICATION NUMBER: US/09/394,457C
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 13
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application...
US-09-394-457C-13

Query Match          1.2%; Score 21.8; DB 4; Length 87;
Best Local Similarity 65.3%; Pred. No. 8e+03;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1334 AGTCCGCTATGGCTTTTAATTCATGACCTTTTGGCTACCTGTGCACTCT 1382
DB      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 AGGCACATATGAATTTTCATTCAGCAGCTTGATGGTGGCGGTGAAGTCT 21

RESULT 44
US-09-709-596A-13/c
; Sequence 13, Application US/09709596A
; Patent No. 6458945
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides
; FILE REFERENCE: 258/239
; CURRENT APPLICATION NUMBER: US/09/709,596A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 13
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application..
US-09-709-596A-13
Query Match      1.2%; Score 21.8; DB 4; Length 87;
Best Local Similarity 65.3%; Pred. No. 8e+03;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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QY 1334 AGTCCGCGTATGCCCTTTAATTCATGACCTTTTGCTACCTGTGCACTCT 1382
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Db 69 AGGACATATGAATTTTCATTTCAGCAGCTTGATGGTCCCGGTGAAGTCT 21
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RESULT 45
US-09-655-104A-13/C
; Sequence 13, Application US/09655104A
; Patent No. 6500650
; GENERAL INFORMATION:
; APPLICANT: Variagenics, Inc.
; TITLE OF INVENTION: A Method for Identifying Polymorphisms
; FILE REFERENCE: 257/078
; CURRENT APPLICATION NUMBER: US/09/655,104A
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence to demonstrate application..
US-09-655-104A-13
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Query Match      1.2%; Score 21.8; DB 4; Length 87;
Best Local Similarity 65.3%; Pred. No. 8e+03;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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QY 1334 AGTCCGCGTATGCCCTTTAATTCATGACCTTTTGCTACCTGTGCACTCT 1382
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 AGGACATATGAATTTTCATTTCAGCAGCTTGATGGTCCCGGTGAAGTCT 21
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Search completed: October 23, 2003, 09:22:31
Job time : 133 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 04:31:57 ; Search time 6720 Seconds
(without alignments)
11347.551 Million cell updates/sec

Title: US-09-868-987-1

Perfect score: 1864

Sequence: 1 atggacttcgcgatattgtc.....atgacaattcagataatgc 1864

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1519770

Minimum DB seq length: 5

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	25.6	1.4	64	11	BX293717	BX293717 Arabidops
2	25.6	1.4	81	6	BD113070	BD113070 EST and e
3	25.6	1.4	81	6	BD113370	BD113370 EST and e
C 4	25.4	1.4	91	14	MAARNA4AX	M10826 Alfalfa mos
C 5	25	1.3	94	6	AX522623	AX522623 Sequence
6	24.8	1.3	94	3	S79433	S79433 cels [5' un
7	24.8	1.3	99	14	AY144374	AY144374 Emiliania
8	24.4	1.3	81	9	HSU81086	U81086 Human immun
9	24.4	1.3	87	11	BX296209	BX296209 Arabidops
10	24.4	1.3	95	6	AR300761	AR300761 Sequence
11	24.4	1.3	95	6	AX089664	AX089664 Sequence
12	24.4	1.3	95	6	AX090119	AX090119 Sequence
13	24.4	1.3	95	6	AX543215	AX543215 Sequence
14	24.2	1.3	97	8	ATH521008	AY521008 Arabidops
15	24.2	1.3	100	8	AY200525	AY200525 Arabidops
C 16	24	1.3	65	6	AX486203	AX486203 Sequence
17	24	1.3	78	6	AR005344	AR005344 Sequence
18	24	1.3	78	6	AR059872	AR059872 Sequence
19	24	1.3	78	6	AR156129	AR156129 Sequence
C 20	23.8	1.3	54	8	ATH522698	AY522698 Arabidops
21	23.8	1.3	87	6	AX435571	AX435571 Sequence
22	23.8	1.3	87	8	AF187253	AF187253 Polytrich
C 23	23.8	1.3	93	8	ATH526349	AJ526349 Arabidops
C 24	23.8	1.3	100	1	LACP1AA	M63184 L.lactis P1
25	23.6	1.3	65	6	AX485729	AX485729 Sequence
C 26	23.6	1.3	72	3	MIAATVR	X03925 Mosquito mi
27	23.6	1.3	79	6	BD035147	BD035147 Sequence
28	23.6	1.3	90	6	AX241109	AX241109 Sequence
C 29	23.6	1.3	98	6	AX326604	AX326604 Sequence
30	23.6	1.3	98	6	AX326665	AX326665 Sequence
C 31	23.4	1.3	88	10	MMGGH3	AF090727 Mus muscu
C 32	23.4	1.3	91	8	YSCWTP041	J01518 Yeast [S.ce
33	23.4	1.3	94	6	BD037934	BD037934 Sequence
34	23.2	1.2	70	6	AX036605	AX036605 Sequence
C 35	23.2	1.2	75	6	BD039479	BD039479 Sequence
36	23.2	1.2	86	8	ATH530983	AJ530983 Arabidops
37	23.2	1.2	91	3	S37388	S37388 Trypanosoma
38	23.2	1.2	96	6	AR140879	AR140879 Sequence
39	23.2	1.2	96	6	AR150829	AR150829 Sequence
40	23.2	1.2	96	6	I65707	I65707 Sequence 67
41	23.2	1.2	96	6	I67939	I67939 Sequence 67
42	23.2	1.2	96	6	I90160	I90160 Sequence 67
C 43	23.2	1.2	98	6	BD115800	BD115800 EST and e
44	23.2	1.2	99	14	AY144376	AY144376 Emiliania
45	23.2	1.2	99	14	AY144377	AY144377 Emiliania

ALIGNMENTS

RESULT 1
BX293717/c
LOCUS
DEFINITION Arabidopsis thaliana transposon insertion STS SM_3.23352, sequence tagged site.
ACCESSION BX293717
VERSION BX293717.1 GI:28949549
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,

JOURNAL
REFERENCE 2 (bases 1 to 64)
AUTHORS Clarke, J.H.
TITLE Direct Submision
JOURNAL Submitted (10-WAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

COMMENT
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon. BBSRC GARNET, ATIS project
On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: DEAD.

FEATURES
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
/db_xref="taxon:3702"
/clone="AC018848"
/note="Derived from superpool 16.28 NASC code N40723"
STS
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/standard_name="SM_3.23352"
BASE COUNT 34 a 3 c 3 g 24 t
ORIGIN

Query Match 1.4%; Score 25.6; DB 11; Length 64;
Best Local Similarity 62.5%; Pred. No. 4.8e+05;
Matches 40; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1020 ACTTCGATATCAACATTTGGATCTTCAGAAAGATCAAAATCTATTTAGTGATAAG 1079
|||||
Db 64 ACTTTTAAATCAATAATGAATTAATAATATAATATATATATTTTGTGTTAGAAA 5
|||||

QY 1080 CTTT 1083
|||||
Db 4 CTTT 1

RESULT 2
BD113070 81 bp DNA linear PAT 18-SEP-2002
LOCUS EST and encoded human protein.
DEFINITION
ACCESSION BD113070
VERSION BD113070.1 GI:23207888
KEYWORDS JP 2002010789-A/5147.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 81)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 5147 15-JAN-2002;
GENSET CORP

OS Homo sapiens (human)
PN JP 2002010789-A/5147
PD 15-JAN-2002
PF 07-AUG-2000 JP 2002080989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..81
/organism="Homo sapiens (human)"
/db_xref="taxon:9606"

FEATURES
source
1..81
/organism="Homo sapiens"
/mol_type="genomic DNA"
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BASE COUNT 16 a 11 c 8 g 46 t
ORIGIN

Query Match 1.4%; Score 25.6; DB 6; Length 81;
Best Local Similarity 57.5%; Pred. No. 4.7e+05;
Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1419 TAGATTGCAAGCCATTTGGTCTTTAAATGACTGTATTGGGGTATTTCATTAAACAATACCTT 1478
|||||
Db 1 TAAATTTTGAGCCCATTTGTACAAATTAAGTCTTTCTGAGAGTATTTTATACCCCTGTAT 60
|||||

QY 1479 TCATCATTTTTCATCGTATT 1498
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Db 61 TTTTCTTCTTTTCTTTTCTTTT 80
|||||

FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 16 a 11 c 8 g 45 t
ORIGIN

Query Match 1.4%; Score 25.6; DB 6; Length 81;
Best Local Similarity 57.5%; Pred. No. 4.7e+05;
Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1419 TAGATTGCAAGCCATTTGGTCTTTAAATGACTGTATTGGGGTATTTCATTAAACAATACCTT 1478
|||||
Db 1 TAAATTTTGAGCCCATTTGTACAAATTAAGTCTTTCTGAGAGTATTTTATACCCCTGTAT 60
|||||

QY 1479 TCATCATTTTTCATCGTATT 1498
|||||
Db 61 TTTTCTTCTTTTCTTTTCTTTT 80
|||||

RESULT 3
BD113370 81 bp DNA linear PAT 18-SEP-2002
LOCUS EST and encoded human protein.
DEFINITION
ACCESSION BD113370
VERSION BD113370.1 GI:23208188
KEYWORDS JP 2002010789-A/5447.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 81)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 5447 15-JAN-2002;
GENSET CORP

OS Homo sapiens (human)
PN JP 2002010789-A/5447
PD 15-JAN-2002
PF 07-AUG-2000 JP 2002080989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..81
/organism="Homo sapiens (human)"
/db_xref="taxon:9606"

FEATURES
source
1..81
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 16 a 11 c 8 g 46 t
ORIGIN

Query Match 1.4%; Score 25.6; DB 6; Length 81;
Best Local Similarity 57.5%; Pred. No. 4.7e+05;
Matches 46; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1419 TAGATTGCAAGCCATTTGGTCTTTAAATGACTGTATTGGGGTATTTCATTAAACAATACCTT 1478
|||||
Db 1 TAAATTTTGAGCCCATTTGTACAAATTAAGTCTTTCTGAGAGTATTTTATACCCCTGTAT 60
|||||

QY 1479 TCATCATTTTTCATCGTATT 1498
|||||
Db 61 TTTTCTTCTTTTCTTTTCTTTT 80
|||||

Db	85	TTCAATTTTAAATACACACACAGTAGGAGTACACTTGGGCACTGTAAACATGTCGTAT 26
Qy	1706	ATTGCACCACTCTGTGTGTG 1726
Db	25	ATACACACAGTATGTGTAG 5
RESULT 6		
LOCUS	S79433	94 bp mRNA linear INV 30-NOV-1995
DEFINITION	celA [5' untranslated region] [Dictyostelium discoideum=slime mold,	
ACCESSION	S79433	
VERSION	S79433.1	GI:1087019
KEYWORDS		
SOURCE	Dictyostelium discoideum	
ORGANISM	Dictyostelium discoideum	
REFERENCE	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.	
AUTHORS	1 (bases 1 to 94)	
TITLE	Ramalingam,R., Blume,J.E., Ganguly,K. and Ennis,H.L.	
	AT-rich upstream sequence elements regulate spore	
	germination-specific expression of the Dictyostelium discoideum	
	celA gene	
JOURNAL	Nucleic Acids Res. 23 (15), 3018-3025 (1995)	
MEDLINE	95388521	
PUBMED	7659526	
REMARK	GenBank staff at the National Library of Medicine created this	
	entry [NCBI gibbsq 170735] from the original journal article.	
	This sequence comes from Table 1.	
FEATURES	Location/Qualifiers	
source	1..94	
	/organism="Dictyostelium discoideum"	
	/mol_type="mRNA"	
	/db_xref="taxon:44689"	
gene	1..94	
	/partial	
	/gene="celA"	
BASE COUNT	24 a 6 c 1 g 63 t	
ORIGIN		
Query Match	1.3%; Score 24.8; DB 3; Length 94;	
Best Local Similarity	60.3%; Pred. No. 7e+05;	
Matches	41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;	
Qy	1600	TCATCATGTTTGTATGCTTTTGTATAGCGGCTCTCTGTCTTTAATTGCAAT 1659
Db	7	TCATCAATTTTCAAAATTTTTTTTATACGATCTTTTTTTTATTATTTT 66
Qy	1660	TATTATGA 1667
Db	67	TTTTTTAA 74
RESULT 7		
LOCUS	AY144374	99 bp DNA linear VRL 07-MAY-2003
DEFINITION	Emiliania huxleyi virus isolate OTU1 major capsid protein (MCP)	
ACCESSION	AY144374	
VERSION	AY144374.1	GI:24429757
KEYWORDS	gene, partial cds.	
SOURCE	Emiliania huxleyi virus	
ORGANISM	Emiliania huxleyi virus	
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae.	
AUTHORS	1 (bases 1 to 99)	
TITLE	Schroeder,D.C., Oke,J., Hall,M., Malin,G. and Wilson,W.H.	
JOURNAL	Virus Succession Observed during an Emiliania huxleyi Bloom	
PUBMED	Appl. Environ. Microbiol. 69 (5), 2484-2490 (2003)	
AUTHORS	2 (bases 1 to 99)	
TITLE	Schroeder,D.C., Oke,J., Hall,M., Evans,C., Malin,G. and Wilson,W.H.	
JOURNAL	Direct Submission	
	Submitted (26-AUG-2002) Marine Biological Association, Citadel	

FEATURES	Hill, Plymouth, Devon PL1 2PB, England	
	Location/Qualifiers	
source	1. .99	
	/organism="Emiliana huxleyi virus"	
gene	/mol_type="genomic DNA"	
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CDS	/db_xref="taxon:181208"	
	complement(<1. .>99)	
CDS	/gene="MCP"	
	complement(<1. .>99)	
CDS	/gene="MCP"	
	/codon_start=1	
CDS	/product="major capsid protein"	
	/protein_id="AA052848.1"	
CDS	/db_xref="GI:24429758"	
	/translation="NQFFTQVQFGAESHTVNRQGDLLSWMYLKIV"	
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	25 g	24 t
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	1.3%; Score 24.8; DB 14; Length 99;	
Query Match	Best Local Similarity 60.3%; Pred. No. 7e+05;	
	Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;	
QY	59	GCAACCGTGGATGGCTGTAGTGATTGACGGTTATATGCTCAGCAGCCCTATT 118
	13	GTACATCCAGTAGCAATCGCTTGACGATTGACGGTAATATGCGACTCAGCCCAA 72
Db	119	TTAAAGCT 126
	73	CTGAAGCT 80
QY		
RESULT 8	HSU81086	
	LOCUS	
DEFINITION	Human immunoglobulin heavy chain CDR3 region (DXP'1) mRNA, partial	
	cds.	
ACCESSION	U81086	
	U81086.1 GI:4098749	
VERSION	Homo sapiens (human)	
	Homo sapiens	
KEYWORDS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
ORGANISM	1 (bases 1 to 81)	
	Keet,M., Mahmoudi,M., Edwards,J.Y., Bell,D.A. and Cairns,E.	
REFERENCE	Direct Submission	
	Submitted (03-DEC-1996) Medicine/Rheumatology, University of	
AUTHORS	Western Ontario, 339 Windermere Road, London, Ontario N6A 5A5,	
	Canada	
JOURNAL	Location/Qualifiers	
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FEATURES	/organism="Homo sapiens"	
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gene	/clone="mah3544"	
	/note="normal individual"	
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CDS	/codon_start=1	
	/product="immunoglobulin heavy chain CDR3 region"	
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	/db_xref="GI:4098750"	
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BASE COUNT	15 a	18 c
	21 g	27 t
ORIGIN		
	1.3%; Score 24.4; DB 9; Length 81;	
Query Match	Best Local Similarity 68.0%; Pred. No. 8.7e+05;	
	Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;	
QY	556	AGGATATACCAAGCGCTTTTGGAGCCATTTTGATTCTTAACCTGACTACAG 605
	1	ATGTTTACTATGTTTCGGGGAGTTATTATGGAITCTACTTTGACTACTG 50
Db		
RESULT 9	BX296209/c	
	LOCUS	
DEFINITION	Arabidopsis thaliana transposon insertion STS SM_3.35057, sequence	
	tagged site.	
ACCESSION	BX296209	
	BX296209.1 GI:29170074	
VERSION	STS; STS, sequence tagged site.	
	Arabidopsis thaliana (thale cress)	
KEYWORDS	Arabidopsis thaliana	
	Arabidopsis thaliana	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
ORGANISM	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE	1	
	Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,	
AUTHORS	Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.	
	Unpublished	
JOURNAL	2 (bases 1 to 87)	
	Clarke,J.H.	
AUTHORS	Direct Submission	
	Submitted (24-MAR-2003) Clarke J.H., John Innes Centre, Colney	
TITLE	Lane, Norwich, NR4 7UJ, UK	
	AT denotes an activation tag dissociation transposon within a	
JOURNAL	single line, ET an enhancer trap dissociation transposon, GT a gene	
	trap dissociation transposon, MT a mis-expression enhancer trap	
COMMENT	dissociation transposon, SM a defective suppressor mutator	
	transposon. _3 denotes a sequence derived from the 3' end of the	
COMMENT	transposon. _5 denotes a sequence derived from the 5' end of the	
	transposon BBSRC GARNET, ATIS project	
COMMENT	On-line seed stock requests: http://nasc.mott.ac.uk/ NASC stock	
	code: N121768.	
FEATURES	Location/Qualifiers	
	1. .87	
source	/organism="Arabidopsis thaliana"	
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source	/variety="Columbia-0 NASC stock code N1092"	
	/db_xref="taxon:3702"	
STS	/clone="AC009918"	
	/note="Derived from superpool 26.44 NASC code Unknown"	
BASE COUNT	54 a	4 c
	12 g	17 t
ORIGIN		
Query Match	1.3%; Score 24.4; DB 11; Length 87;	
	Best Local Similarity 60.6%; Pred. No. 8.6e+05;	
Matches	40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	
QY	1597	AACTCTATCAGTTTGTAAATGCTTTTATAGCGCGCTCTCTGCTTTAAATTTGC 1656
	80	AACTTATTCGTTTTTATATATTTTTTTTCTATTTTTTTTACTTTTCTTAATCTGA 21
Db		
QY	1657	ATTAT 1662
Db		
RESULT 10	AR300761	
	LOCUS	
DEFINITION	Sequence 13 from patent US 6537972.	
	AR300761	
ACCESSION	AR300761	
	VERSION	
KEYWORDS	AR300761.1 GI:31688328	
	Unknown.	
SOURCE	Unknown.	
	Unclassified.	
ORGANISM		

REFERENCE 1 (bases 1 to 95)
AUTHORS Holzmayer,T.A., Dunn,S.J. and Dayn,A.
TITLE Compositions and methods for inhibiting human immunodeficiency virus infection by down-regulating human cellular genes
JOURNAL Patent: US 6537972-A 13 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..95
BASE COUNT 28 a 15 c 13 g 39 t
ORIGIN
Query Match 1.3%; Score 24.4; DB 6; Length 95;
Best Local Similarity 58.1%; Pred. No. 8.6e+05;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 791 AACCATGATTTCTTGAGAGGATGCAAAAACCTTTGGCTGTTTCTGGAAGTGTTCCTT 850
Db 14 AAGCATGACCTTTTATACATGGAATAAATTATGCAATTTCTATTGAAATTTCAACGCT 73
QY 851 TTAGGTTCGTTGC 864
Db 74 TTGTTTCTTTGGC 87
RESULT 11
LOCUS AX089664 95 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 13 from Patent WO0116322.
ACCESSION AX089664
VERSION AX089664.1 GI:13443846
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Holzmayer,T.A. and Dunn,S.J.
TITLE Compositions and methods for inhibiting human immunodeficiency virus infection by down-regulating human cellular genes
JOURNAL Patent: WO 0116322-A 13 08-MAR-2001;
Subsidiary N0. 3, INC. (US)
FEATURES Location/Qualifiers
source 1..95
BASE COUNT 28 a 15 c 13 g 39 t
ORIGIN
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Best Local Similarity 58.1%; Pred. No. 8.6e+05;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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Db 14 AAGCATGACCTTTTATACATGGAATAAATTATGCAATTTCTATTGAAATTTCAACGCT 73
QY 851 TTAGGTTCGTTGC 864
Db 74 TTGTTTCTTTGGC 87
RESULT 12
LOCUS AX090119 95 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 13 from Patent WO0116323.
ACCESSION AX090119
VERSION AX090119.1 GI:13444080
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Holzmayer,T.A. and Dunn,S.J.
TITLE Compositions and methods for inhibiting human immunodeficiency virus infection by down-regulating human cellular genes
JOURNAL Patent: WO 0116322-A 13 08-MAR-2001;
Subsidiary N0. 3, INC. (US)
FEATURES Location/Qualifiers
source 1..95
BASE COUNT 28 a 15 c 13 g 39 t
ORIGIN
Query Match 1.3%; Score 24.4; DB 6; Length 95;
Best Local Similarity 58.1%; Pred. No. 8.6e+05;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 791 AACCATGATTTCTTGAGAGGATGCAAAAACCTTTGGCTGTTTCTGGAAGTGTTCCTT 850
Db 14 AAGCATGACCTTTTATACATGGAATAAATTATGCAATTTCTATTGAAATTTCAACGCT 73
QY 851 TTAGGTTCGTTGC 864
Db 74 TTGTTTCTTTGGC 87

REFERENCE 1
AUTHORS Holzmayer,T.A. and Dunn,S.J.
TITLE Compositions and methods for inhibiting human immunodeficiency virus infection by down-regulating human cellular genes
JOURNAL Patent: WO 0116323-A 13 08-MAR-2001;
Subsidiary N0. 3, INC. (US)
FEATURES Location/Qualifiers
source 1..95
BASE COUNT 28 a 15 c 13 g 39 t
ORIGIN
Query Match 1.3%; Score 24.4; DB 6; Length 95;
Best Local Similarity 58.1%; Pred. No. 8.6e+05;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 791 AACCATGATTTCTTGAGAGGATGCAAAAACCTTTGGCTGTTTCTGGAAGTGTTCCTT 850
Db 14 AAGCATGACCTTTTATACATGGAATAAATTATGCAATTTCTATTGAAATTTCAACGCT 73
QY 851 TTAGGTTCGTTGC 864
Db 74 TTGTTTCTTTGGC 87
RESULT 13
LOCUS AX543215 95 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 13 from Patent WO0244722.
ACCESSION AX543215
VERSION AX543215.1 GI:25276515
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Holzmayer,T.A. and Dunn,S.J.
TITLE Compositions and methods for inhibiting human immunodeficiency virus infection by down-regulating human cellular genes
JOURNAL Patent: WO 0244722-A 13 06-JUN-2002;
Subsidiary N0. 3, INC. (US)
FEATURES Location/Qualifiers
source 1..95
BASE COUNT 28 a 15 c 13 g 39 t
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Query Match 1.3%; Score 24.4; DB 6; Length 95;
Best Local Similarity 58.1%; Pred. No. 8.6e+05;
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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Db 14 AAGCATGACCTTTTATACATGGAATAAATTATGCAATTTCTATTGAAATTTCAACGCT 73
QY 851 TTAGGTTCGTTGC 864
Db 74 TTGTTTCTTTGGC 87
RESULT 14
LOCUS ATH521008 97 bp DNA linear PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone OS0C12.
ACCESSION AJ521008
VERSION AJ521008.1 GI:26789244
KEYWORDS left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1

TITLE Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
JOURNAL Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
MEDLINE Lepiniec, L., Caboche, M., and Lecharny, A.
22363535 1-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

REFERENCE PUBMED 12446565
2 (bases 1 to 97)
AUTHORS Balzerque, S.
JOURNAL Direct Submission
TITLE Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.inbio.gen.fr).

FEATURES
source
1..97
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="WassiljewskiJa"
/db_xref="taxon:3702"
/clone="050C12"
misc_feature 1..97
/clone.lib="Arabidopsis thaliana T-DNA insertion lines"
/note="T-DNA flanking sequence
left border"
BASE COUNT 26 a 21 c 29 g 21 t
ORIGIN

Query Match 1.3%; Score 24.2; DB 8; Length 97;
Best Local Similarity 66.08; Pred. No. 9.5e+05;
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 322 TGTATTCATGAGCGTATATTATGATTGGAGCGTCATCGCTTCGGAGCTG 374
1
Db 10 TGATTTGATCACGTGTATGATTGATTAAAGGCGGTCAGACCTAGGTAGGATG 62

RESULT 15
AY200525 100 bp DNA linear PLN 24-JAN-2003
LOCUS Arabidopsis thaliana sequence flanking Ds3 end of Ds-EnhancerTrap
DEFINITION Insertion from line ET8745.
ACCESSION AY200525
VERSION AY200525.1 GI:27896479
KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 100)
May, B.P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,
McCombie, W.R. and Martienssen, R.A.
Arabidopsis genomic sequences flanking Ds enhancer and gene traps
in transgenic lines
Unpublished
2 (bases 1 to 100)

AUTHORS May, B.P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,
McCombie, W.R. and Martienssen, R.A.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-2002) Cold Spring Harbor Laboratory, 1 Bungtown
Road, Cold Spring Harbor, NY 11724, USA
COMMENT http://genetrap.cshl.org.
FEATURES
source
1..100
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="ET8745.Ds3.07.21.2001.jw03.100"
/note="transgenic line ET8745
ecotype: Landsberg"
BASE COUNT 29 a 23 c 10 g 38 t
ORIGIN

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Best Local Similarity 62.3%; Pred. No. 9.4e+05;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1351 AATTCATGACCTTTGGCTACCTGCGAGCTCTTTATAGCAGATTTCTTTTGAAGAA 1410
1
Db 21 AACTTATAAACTGTGTCATATCATGCTCTCTTTTAAATAACCTTTCTTTTGGCGCA 80

QY 1411 A 1411
Db 81 A 81

RESULT 16
AX486203/c 65 bp DNA linear PAT 16-AUG-2002
LOCUS AX486203
DEFINITION Sequence 3503 from Patent WO02053728.
ACCESSION AX486203
VERSION AX486203.1 GI:22320419
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

REFERENCE 1
AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 3503 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
1..65
/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
BASE COUNT 26 a 12 c 8 g 19 t
ORIGIN

Query Match 1.3%; Score 24; DB 6; Length 65;
Best Local Similarity 60.9%; Pred. No. 1.1e+06;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1684 AGGAACCTTATCGTCTCTTTATATTATGACCACTCTGTTGTTTATGTCGTAAGA 1743
1
Db 65 ATGGATTTTAGCCTCTCATATATTTAAACGCGTTTGTATGTTGAAGGATTATCAATA 6

QY 1744 AAAT 1747
1
Db 5 GAGT 2

RESULT 17
AR005344 78 bp DNA linear PAT 04-DEC-1998
LOCUS AR005344
DEFINITION Sequence 22 from patent US 5747662.
ACCESSION AR005344
VERSION AR005344.1 GI:3966223

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 78)
 AUTHORS Simmons,L.C. and Yansura,D.G.
 TITLE Methods and compositions for secretion of heterologous polypeptides
 JOURNAL Patent: US 5747662-A 22 05-MAY-1998;
 FEATURES
 Location/Qualifiers
 1..78
 /organism="unknown"
 BASE COUNT 21 a 14 c 12 g 30 t 1 others
 ORIGIN
 Query Match 1.3%; Score 24; DB 6; Length 78;
 Best Local Similarity 64.3%; Pred. No. 1.1e+06;
 Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1659 TTATTATGACCATAGGATCTCTTAGGAACCTTTATCGTCTCTTTATATGACCA 1714
 Db 11 TGAAGAAAGAACATAGCGTTCTCTTGTCATCTATGTTTCGTTTTCTATTGCTACA 66
 RESULT 18
 AR059872
 LOCUS
 DEFINITION Sequence 22 from patent US 5840523.
 ACCESSION AR059872
 VERSION AR059872.1 GI:5986322
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 78)
 AUTHORS Simmons,L.C. and Yansura,D.G.
 TITLE Methods and compositions for secretion of heterologous polypeptides
 JOURNAL Patent: US 5840523-A 22 24-NOV-1998;
 FEATURES
 Location/Qualifiers
 1..78
 /organism="unknown"
 BASE COUNT 21 a 14 c 12 g 30 t 1 others
 ORIGIN
 Query Match 1.3%; Score 24; DB 6; Length 78;
 Best Local Similarity 64.3%; Pred. No. 1.1e+06;
 Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1659 TTATTATGACCATAGGATCTCTTAGGAACCTTTATCGTCTCTTTATATGACCA 1714
 Db 11 TGAAGAAAGAACATAGCGTTCTCTTGTCATCTATGTTTCGTTTTCTATTGCTACA 66
 RESULT 19
 AR156129
 LOCUS
 DEFINITION Sequence 22 from patent US 6242177.
 ACCESSION AR156129
 VERSION AR156129.1 GI:15124833
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 78)
 AUTHORS Simmons,L.C. and Yansura,D.G.
 TITLE Methods and compositions for secretion of heterologous polypeptides
 JOURNAL Patent: US 6242177-A 22 05-JUN-2001;
 FEATURES
 Location/Qualifiers
 1..78
 /organism="unknown"
 BASE COUNT 21 a 14 c 12 g 30 t 1 others
 ORIGIN
 Query Match 1.3%; Score 24; DB 6; Length 78;
 Best Local Similarity 64.3%; Pred. No. 1.1e+06;
 Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1659 TTATTATGACCATAGGATCTCTTAGGAACCTTTATCGTCTCTTTATATGACCA 1714
 Db 11 TGAAGAAAGAACATAGCGTTCTCTTGTCATCTATGTTTCGTTTTCTATTGCTACA 66
 RESULT 19
 AR156129
 LOCUS
 DEFINITION Sequence 22 from patent US 6242177.
 ACCESSION AR156129
 VERSION AR156129.1 GI:15124833
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 78)
 AUTHORS Simmons,L.C. and Yansura,D.G.
 TITLE Methods and compositions for secretion of heterologous polypeptides
 JOURNAL Patent: US 6242177-A 22 05-JUN-2001;
 FEATURES
 Location/Qualifiers
 1..78
 /organism="unknown"
 BASE COUNT 21 a 14 c 12 g 30 t 1 others
 ORIGIN
 Query Match 1.3%; Score 24; DB 6; Length 78;
 Best Local Similarity 64.3%; Pred. No. 1.1e+06;
 Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1659 TTATTATGACCATAGGATCTCTTAGGAACCTTTATCGTCTCTTTATATGACCA 1714
 Db 11 TGAAGAAAGAACATAGCGTTCTCTTGTCATCTATGTTTCGTTTTCTATTGCTACA 66

Best Local Similarity 64.3%; Pred. No. 1.1e+06;
 Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1659 TTATTATGACCATAGGATCTCTTAGGAACCTTTATCGTCTCTTTATATGACCA 1714
 Db 11 TGAAGAAAGAACATAGCGTTCTCTTGTCATCTATGTTTCGTTTTCTATTGCTACA 66
 RESULT 20
 ATH522698
 LOCUS
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 297A10.
 ACCESSION AJ522698
 VERSION AJ522698.1 GI:26790934
 KEYWORDS left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
 1
 AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Sanson, P., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 MEDLINE 22363535
 PUBMED 12446565
 REFERENCE
 2 (bases 1 to 54)
 AUTHORS Balzergue, S.
 TITLE Direct Submission
 JOURNAL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
 FEATURES
 Location/Qualifiers
 1..54
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 /mol_type="genomic DNA"
 /cultivar="Wassillewskija"
 /db_xref="taxon:3702"
 /clone="297A10"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 misc_feature
 1..54
 /note="T-DNA flanking sequence left border"
 BASE COUNT 23 a 3 c 6 g 22 t
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 Query Match 1.3%; Score 23.8; DB 8; Length 54;
 Best Local Similarity 72.1%; Pred. No. 1.2e+06;
 Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1588 AACAGTACAACCTCTATCATGTTTGTATGCTTTTGTATATA 1630
 Db 54 AAAAAATACAAAATTATCATCTTTTGCATATGCTTTTTCGATA 12
 RESULT 21
 AX435571
 LOCUS
 DEFINITION Sequence 3986 from Patent WO0229113.
 Query Match 1.3%; Score 23.8; DB 8; Length 54;
 Best Local Similarity 72.1%; Pred. No. 1.2e+06;
 Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1588 AACAGTACAACCTCTATCATGTTTGTATGCTTTTGTATATA 1630
 Db 54 AAAAAATACAAAATTATCATCTTTTGCATATGCTTTTTCGATA 12

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ACCESSION AX435571
VERSION AX435571.1 GI:21660379
SOURCE Bacillus licheniformis
ORGANISM Bacillus licheniformis
REFERENCE 1
AUTHORS Berka, R. and Clausen, I. G.
TITLE Methods for monitoring multiple gene expression
JOURNAL Patent: WO 0229113-A 3986 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S (DK)
FEATURES
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        1..87
            /organism="Bacillus licheniformis"
            /mol_type="genomic DNA"
            /db_xref="taxon:11402"
BASE COUNT 15 a 18 c 25 g 29 t
ORIGIN
Query Match 1.3%; Score 23.8; DB 6; Length 87;
Best Local Similarity 59.7%; Pred. No. 1.2e+06;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 331 GAGCGTATATTAGATTTGGAGCGTCATCGCTCGGAGCTGTCTCTGAATCTTT 390
Db 1 GAGCGAGGTTACGGACACGAGCGTTTGCTTAATTGTTCTGTCTATCTCTT 60

QY 391 GCTTATC 397
Db 61 AATCATC 67

RESULT 22
AF187253
LOCUS
DEFINITION Polytrichadelphus magellanicus trnL-trnF intergenic spacer,
chloroplast sequence.
ACCESSION AF187253
VERSION AF187253.1 GI:15592942
KEYWORDS chloroplast Polytrichadelphus magellanicus
ORGANISM Polytrichadelphus magellanicus
REFERENCE 1
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Bryophyta;
Polytrichopsida; Polytrichales; Polytrichaceae; Polytrichadelphus.
TITLE 1 (bases 1 to 87)
JOURNAL Quandt, D.
REFERENCE 2
AUTHORS Molecular divergence of New Zealand samples of Meteoriaceae and
Lembophyllaceae
JOURNAL Quandt, D.
REFERENCE 2 (bases 1 to 87)
AUTHORS Direct Submission
TITLE Submitted (16-SEP-1999) Institut fuer Biologie-Systematische
JOURNAL Botanik und Pflanzengographie, Freie Universitaet Berlin,
Altensteinsrasse 6, Berlin 14195, Germany
FEATURES
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            /organism="Polytrichadelphus magellanicus"
            /organelle="plastid:chloroplast"
            /mol_type="genomic DNA"
            /db_xref="taxon:111667"
    misc_feature 1..87
        /note="trnL-trnF intergenic spacer"
BASE COUNT 42 a 3 c 6 g 36 t
ORIGIN
Query Match 1.3%; Score 23.8; DB 8; Length 87;
Best Local Similarity 62.7%; Pred. No. 1.2e+06;
Matches 37; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1033 AACATTGGATCTTCAGAAAGATCAAAATCTATTTTAGTGATPAAAGCTTTAAGCTATA 1091
Db 1 AAAATTATATAAGAAAAAATAAATTCATTTCATTTTATTGACATAAGTTAATTTTA 59

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RESULT 23
ATH526349/c
LOCUS
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
118E10.
ACCESSION AJ526349
VERSION AJ526349.1 GI:26794609
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 93)
AUTHORS Balzergue, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..93
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassiljewskaja"
            /db_xref="taxon:3702"
            /clone="118E10"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    misc_feature 1..93
        /note="T-DNA flanking sequence
        left border"
BASE COUNT 47 a 8 c 11 g 27 t
ORIGIN
Query Match 1.3%; Score 23.8; DB 8; Length 93;
Best Local Similarity 53.8%; Pred. No. 1.2e+06;
Matches 49; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 816 AAAAATTGGCTCTTTCTGGAAGTGTTCCTTTTCTTTAGTTGCGTCTCTCGGGTTG 875
Db 93 AAAACAATCTTCGCTTTTCACTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 34

QY 876 GAGCTCGAATCCGTTTGGGAATGGATT 906
Db 33 GTTATTTGAATTGATATTAATAAATAATTT 3

RESULT 24
LACPIAA/c
LOCUS
DEFINITION L.lactis P1 promoter, partial sequence.
ACCESSION M63184
VERSION M63184.1 GI:149458

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KEYWORDS      Lactococcus lactis
SOURCE        Lactococcus lactis
ORGANISM      Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
              Lactococcus.
REFERENCE     1 (bases 1 to 100)
AUTHORS       Koivula,T., Sibakov,M. and Palva,I.
TITLE         Isolation and Characterization of Lactococcus lactis subsp. lactis
              promoters
JOURNAL       Appl. Environ. Microbiol. 57 (2), 333-340 (1991)
MEDLINE       91197100
PUBMED        1707605
COMMENT       Original source text: L.lactis, cDNA to mRNA.
FEATURES      Location/Qualifiers
               1..100
               /organism="Lactococcus lactis"
               /mol_type="genomic DNA"
               /db_xref="taxon:1358"
               1..100
               /partial
               /note="pl"
BASE COUNT    43 a 11 c 17 g 29 t
ORIGIN
Query Match   1.3%; Score 23.8; DB 1; Length 100;
Best Local Similarity 59.7%; Pred. No. 1.2e+06;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1389 TAGCACATTCCTTTTGAGAAAATTCAAATAGATTGCAAGCCATTGGCTTTAATGA 1448
      |||||
DB 94 TCGGACTTATGATTATTTAGCATTTTTCACAAATGCAAGTCTTTTCATAAAGC 35
      |||||
QY 1449 CTGTATT 1455
      |||||
DB 34 CTTTATT 28

RESULT 25
AX485729      65 bp DNA linear PAT 16-AUG-2002
LOCUS         Sequence 3029 from Patent WO02053728.
DEFINITION
ACCESSION     AX485729
VERSION       AX485729.1 GI:22319945
KEYWORDS      Candida albicans
SOURCE        Candida albicans
ORGANISM      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
              Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE     1
AUTHORS       Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE         Gene disruption methodologies for drug target discovery
JOURNAL       Patent: WO 02053728-A 3029 11-JUL-2002;
              Eliira Pharmaceuticals, Inc. (US)
FEATURES      Location/Qualifiers
               1..65
               /organism="Candida albicans"
               /mol_type="genomic DNA"
               /db_xref="taxon:5476"
BASE COUNT    21 a 7 c 18 g 19 t
ORIGIN
Query Match   1.3%; Score 23.6; DB 6; Length 65;
Best Local Similarity 69.6%; Pred. No. 1.3e+06;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 268 AAAACAATGACAAAGGCAATTCACAGATCTGTGGCTGGCA 313
      |||||
DB 19 AAAGCAATGTATAAAGGCTTGTATAGGATGCTGTACATTAGCA 64
      |||||

RESULT 26
MIAATVR/c    72 bp DNA linear INV 11-JUN-2003
LOCUS         MIAATVR/c
DEFINITION    Sequence tag and encoded human protein.

```

```

DEFINITION    Mosquito mitochondrial tRNA-Val (UAC).
ACCESSION     X03925
VERSION       X03925.1 GI:12641
KEYWORDS      transfer RNA; transfer RNA-Val.
SOURCE        mitochondrion Aedes albopictus (Asian tiger mosquito)
ORGANISM      Aedes albopictus
REFERENCE     1 (bases 1 to 72)
AUTHORS       Dubin,D.T., HsuChen,C.C. and Tillotson,L.E.
TITLE         Mosquito mitochondrial transfer RNAs for valine, glycine and
              glutamate: RNA and gene sequences and vicinal genome organization
JOURNAL       Curr. Genet. 10 (9), 701-707 (1986)
MEDLINE       88194654
COMMENT       Data kindly reviewed (06-OCT-1986) by D. Dubin.
FEATURES      Location/Qualifiers
               1..72
               /organism="Aedes albopictus"
               /organelle="mitochondrion"
               /mol_type="genomic DNA"
               /db_xref="taxon:7160"
               1..72
               /product="tRNA-Val"
               9
               /note="1-methyladenosine"
               /mod_base=m1a
               10
               /note="2-methylguanosine"
               /mod_base=m2g
               27
               /note="pseudouridine"
               /mod_base=p
               28
               /note="pseudouridine"
               /mod_base=p
               34..36
               /note="anticodon UAC"
               37
               /note="N-(9-beta-D-ribofuranosylpurine-6-yl) carbamoyl)
               threonine in tRNA-Val"
               /mod_base=OTHER
               38
               /note="pseudouridine"
               /mod_base=p
               39
               /note="pseudouridine"
               /mod_base=p
               64
               /note="pseudouridine"
               /mod_base=p
               65
               /note="pseudouridine"
               /mod_base=p
BASE COUNT    31 a 8 g 27 t
ORIGIN
Query Match   1.3%; Score 23.6; DB 3; Length 72;
Best Local Similarity 61.3%; Pred. No. 1.3e+06;
Matches 38; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 662 TTGACATTGATTTAGGAATTTCTCTCAATGTTTACGGCTCTTTTCATGACTAAATTT 721
      |||||
DB 68 TTAAATGATTTCACAAATTTCTTTCAATGTAATGAAATACTTTTACTAATTAAGCT 9
      |||||
QY 722 TT 723
      ||
DB 8 TT 7

RESULT 27
BD035147      79 bp DNA linear PAT 27-AUG-2002
LOCUS         BD035147
DEFINITION    Sequence tag and encoded human protein.

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ACCESSION BD035147
VERSION BD035147.1 GI:22576889
KEYWORDS JP 2001269182-A/11393.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 79)
AUTHORS Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 11393 02-OCT-2001;
GENSET OS Homo sapiens (human)
COMMENT PN JP 2001269182-A/11393
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09.C07K14/435.C07K16/18.C12N1/15.C12N1/19.C12N1/21, PC
C12N5/10
PC C12P21/02.C12P21/08.C12Q1/68//G06F17/30.C12N15/00.C12N5/00, PC
CC G06F15/40
PH Key Location/Qualifiers.
source 1..79
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606" 32 t
BASE COUNT 22 a 11 c 14 g
ORIGIN
Query Match 1.3%; Score 23.6; DB 6; Length 79;
Best Local Similarity 69.6%; Pred. No. 1.3e+06;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1348 TTTAATTCATGACCTTTGGCTACCTGTGACGCTCTGTTTATAGCA 1393
|||||
Db 3 TTTAATTCATGACCTTTGGCTACCTGTGACGCTCTGTTTATAGCA 48
RESULT 28
AX241109
LOCUS 90 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 347 from Patent WO0160975.
ACCESSION AX241109
VERSION AX241109.1 GI:15797984
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Roemer,T., Jiang,B., Boone,C. and Bussey,H.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 0160975-A 347 23-AUG-2001;
Elitra Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..90
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="DNA primer" 28 t
BASE COUNT 27 a 10 c 25 g
ORIGIN
Query Match 1.3%; Score 23.6; DB 6; Length 90;
Best Local Similarity 69.6%; Pred. No. 1.3e+06;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 268 AAACAATGTACACAGGCAATATCTCAGCATGCTGTGGCTTGGCA 313
|||||
Db 19 AAACAATGTATAAAGGCTTGTGATAGGATGCTGTACATTAGCA 64

RESULT 29
AX326604/c
LOCUS 98 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 25 from Patent WO0192579.
ACCESSION AX326604
VERSION AX326604.1 GI:18097367
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wenz,H.M. and Schroth,G.P.
TITLE Methods for detecting target nucleic acids using coupled ligation
JOURNAL Patent: WO 0192579-A 25 06-DEC-2001;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1..98
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="allele of SEQ ID NO: 24; pivotal nucleotide (49)"
BASE COUNT 23 a 15 c 20 g 40 t
ORIGIN
Query Match 1.3%; Score 23.6; DB 6; Length 98;
Best Local Similarity 58.6%; Pred. No. 1.3e+06;
Matches 41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1156 TGTGAGAACAGCGCTAGATTCTCTACGGAACCTCTAAACGAAACGCAAAATTTTGGTC 1215
|||||
Db 77 TGTGAGAACAGCGCTAGATTCTCTACGGAACCTCTAAACGAAACGCAAAATTTTGGTC 18
QY 1216 AAAGGTAAGC 1225
|||||
Db 17 AAAGGTAAGC 8
RESULT 30
AX326665
LOCUS 98 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 86 from Patent WO0192579.
ACCESSION AX326665
VERSION AX326665.1 GI:18097428
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wenz,H.M. and Schroth,G.P.
TITLE Methods for detecting target nucleic acids using coupled ligation
JOURNAL Patent: WO 0192579-A 86 06-DEC-2001;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1..98
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="complement of SEQ ID NO: 25"
BASE COUNT 40 a 20 c 15 g 23 t
ORIGIN
Query Match 1.3%; Score 23.6; DB 6; Length 98;
Best Local Similarity 58.6%; Pred. No. 1.3e+06;
Matches 41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1156 TGTGAGAACAGCGCTAGATTCTCTACGGAACCTCTAAACGAAACGCAAAATTTTGGTC 1215
|||||

Db 22 TGTACGACACCCATGTATCCATATACGGCAATCAATAAGGAACCTATGACCTAAAGC 81

Qy 1216 AAAGCTAAGC 1225

Db 82 AAAGCTAAGC 91

RESULT 31
MMGGH3/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM

MMGGH3
Mus musculus gamma-glutamyl hydrolase gene, exon 3.
AF090727
AF090727.1 GI:5712212

3 of 8
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE

Esaki, T., Roy, K., Yao, R., Galivan, J. and Sirotnak, F.M.
Cloning of mouse gamma-glutamyl hydrolase in the form of two cDNA
variants with different 5' ends and encoding alternate leader
peptide sequences
Gene 219 (1-2), 37-44 (1998)

JOURNAL
MEDLINE
PUBMED

98434456
9756990

REFERENCE
AUTHORS
TITLE

Esaki, T., Masumoto, N., Hayes, P., Chen, J. and Sirotnak, F.M.
Organization and structure of the mouse gamma-glutamyl hydrolase
gene and the functional identification of its promoter
Gene 234 (1), 93-100 (1999)

JOURNAL
MEDLINE
PUBMED

10393243

REFERENCE
AUTHORS
TITLE

Masumoto, N., Esaki, T. and Sirotnak, F.M.
Additional organizational features of the murine gamma-glutamyl
hydrolase gene. Two remotely situated exons within the complement
C3 gene locus encode an alternate 5' end and proximal ORF under the
control of a bidirectional promoter
Gene 268 (1-2), 183-194 (2001)

JOURNAL
MEDLINE
PUBMED

21261955
11368914

REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (09-SEP-1998) Molecular Therapeutics, Memorial
Sloan-Kettering Cancer Center, 1275 York Avenue, New York, NY
10021, USA

FEATURES
source

Location/Qualifiers
1. .88
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129/SVJ"
/db_xref="taxon:10090"
20. .70
/number=3
21 a 11 c 21 g 35 t

BASE COUNT
ORIGIN

Query Match 1.3%; Score 23.4; DB 10; Length 88;
Best Local Similarity 63.2%; Pred. No. 1.4e+06;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 714 CTAATTTTCTTCATCGTGTGATGAATAGACCAACATACACAGTTGCATATGA 770

Db 58 CTAATAAGTTCTTACTACTCTCATCTAGAGCTGAGGCTGAAACACAGGAATGA 2

RESULT 32
YSCWTP041/c

LOCUS
DEFINITION

YSCWTP041
Yeast (S.cerevisiae) mitochondrial petite mutant excision seq 4,

left end.

J01518
J01518.1 GI:343852

AT-rich region; GC rich region.

1 of 2

mitochondrion Saccharomyces cerevisiae (baker's yeast)

ORGANISM
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

1 (bases 1 to 91)
de Zamaroczy, M., Faugeron-Ponty, G. and Bernardi, G.
Excision sequences in the mitochondrial genome of yeast
Gene 21 (3), 193-202 (1983)

6343188
63210931

Original source text: Yeast (Saccharomyces cerevisiae)
mitochondrial DNA.
Additional sequences reported in [1], but sequenced in earlier
papers, appear in separate entries. Excision repeat corresponds to
bases 35 to 39.

FEATURES
source

Location/Qualifiers
1. .91
/organism="Saccharomyces cerevisiae"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/db_xref="taxon:4932"
52 a 0 c 2 g 37 t

BASE COUNT
ORIGIN

Query Match 1.3%; Score 23.4; DB 8; Length 91;
Best Local Similarity 55.6%; Pred. No. 1.4e+06;
Matches 45; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 1009 TTCTCTAGAGACTTCGCTATTCAACATTTGGATCTTCAGAAAAGATCAAAATCTATT 1068

Db 81 TTATTTATATATATTTATTTATATAAATATTAATCTATTATATAAATTTATATAATATAT 22

Qy 1069 TAGTGATAAAGCTTTAAAGCTA 1089

Db 21 TTAATATATTTCTTTAAATTA 1

RESULT 33
BD037934

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD037934
Sequence tag and encoded human protein.
BD037934
BD037934.1 GI:22579676
JP 2001269182-A/14180.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 94)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 14180 02-OCT-2001;
GENSET

OS Homo sapiens (human)
PN JP 2001269182-A/14180
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40

CC
FH Key Location/Qualifiers
1. .94

FEATURES
source

Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
19 a      8 c      13 g      52 t      2 others
BASE COUNT
ORIGIN
Query Match      1.3%; Score 23.4; DB 6; Length 94;
Best Local Similarity 63.2%; Pred. No. 1.4e+06;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1348 TTTAATTCATGACCTTTGGCTACCTGTGCGAGTCTTTGTTATAGCACATCTCTTTT 1404
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
26 TTTTATGTTATCCTTTATGCACTTATAATGTTCTTTTATAGGATCTCTTTT 82
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 34
AX036605
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
MERISTEM THERAPEUTICS (FR)
Location/Qualifiers
FEATURES
source
1. .70
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Directional building block SI"
BASE COUNT 26 a 18 c 10 g 16 t
ORIGIN

Query Match      1.2%; Score 23.2; DB 6; Length 70;
Best Local Similarity 61.7%; Pred. No. 1.6e+06;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1029 TTCAACATTTGGATCTTCAGAAAGATCAAAATCTATTTCAGTATAAGCTTTAAGCT 1088
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
6 TTCAACACATACAAATTCAGTAGAGAACTATTACTCTTGAGAAACCTAGAGGAT 55
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 35
BD039479/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/15725
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PC C12N15/09, C07K14/435, C07K16/19, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC

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G06F15/40
CC
FH Key' Location/Qualifiers
FEATURES
source
1. .75
Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"
19 a      7 c      13 g      36 t
BASE COUNT
ORIGIN
Query Match      1.2%; Score 23.2; DB 6; Length 75;
Best Local Similarity 61.7%; Pred. No. 1.6e+06;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1160 AGAAACAGCCCTAGATTTCTCTACGAAACTTAAACGMAAGCGAAATTTGGTCAAAG 1219
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
70 AAAAAAATACATGATTTCTCTATGGATATGCCACATACCCATATATCTTAAGTCAAAG 11
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 36
ATH530983
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.inbio.gen.fr).
Location/Qualifiers
1. .86
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="222F11"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .86
/notes="T-DNA flanking sequence
left border"
BASE COUNT 46 a 7 c 9 g 24 t
ORIGIN
Query Match      1.2%; Score 23.2; DB 8; Length 86;

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RESULT 43

source 1..99
 /organism="Emiliania huxleyi virus"
 /mol_type="genomic DNA"
 /isolate="OTU3"
 /db_xref="taxon:181208"
 complement(<1..>99)
 /gene="MCP"
 complement(<1..>99)
 /gene="MCP"
 /codon_start=1
 /product="major capsid protein"
 /protein_id="AA052850.1"
 /db_xref="GI:24429762"
 /translation="NQPFVTQVQGAESHITVNRQDLSWMYLKIV"
 BASE COUNT 28 a 23 c 23 g 25 t
 ORIGIN

Query Match 1.2%; Score 23.2; DB 14; Length 99;
 Best Local Similarity 58.8%; Pred. No. 1.6e+06;
 Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 59 GCAAAACCGTGGATGCGTATGCTGTAGTGATTGACGGTTATATGTCAGCAGCCCTATT 118
 Db 13 GTACATCCACGATAGCAAAATCGCCTTGACGGTTGACGGTAATATCGGACTCAGCCCCAAA 72

QY 119 TTAAACGT 126
 Db 73 CTGAACCT 80

RESULT 45
 AY144377
 LOCUS
 DEFINITION Emiliania huxleyi virus isolate OTU4 major capsid protein (MCP)
 ACCESSION AY144377.
 VERSION AY144377.1 GI:24429763
 KEYWORDS
 SOURCE Emiliania huxleyi virus
 ORGANISM Emiliania huxleyi virus
 Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae.
 REFERENCE 1 (bases 1 to 99)
 Schroeder,D.C., Oke,J., Hall,M., Malin,G. and Wilson,W.H.
 TITLE Virus Succession Observed during an Emiliania huxleyi Bloom
 JOURNAL Appl. Environ. Microbiol. 69 (5), 2484-2490 (2003)
 PUBMED 12732512
 REFERENCE 2 (bases 1 to 99)
 Schroeder,D.C., Oke,J., Hall,M., Evans,C., Malin,G. and Wilson,W.H.
 AUTHORS Direct Submission
 TITLE Submitted (26-AUG-2002) Marine Biological Association, Citadel
 JOURNAL Hill, Plymouth, Devon PL1 2PB, England
 FEATURES
 Location/Qualifiers

1..99
 /organism="Emiliania huxleyi virus"
 /mol_type="genomic DNA"
 /isolate="OTU4"
 /db_xref="taxon:181208"
 complement(<1..>99)
 /gene="MCP"
 complement(<1..>99)
 /gene="MCP"
 /codon_start=1
 /product="major capsid protein"
 /protein_id="AA052851.1"
 /db_xref="GI:24429764"
 /translation="NQPFVTQVQGAESHITVNRQDLSWMYLKIV"
 BASE COUNT 26 a 23 c 25 g 24 t 1 others
 ORIGIN

Query Match 1.2%; Score 23.2; DB 14; Length 99;
 Best Local Similarity 58.8%; Pred. No. 1.6e+06;
 Matches 40; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 59 GCAAAACCGTGGATGCGTATGCTGTAGTGATTGACGGTTATATGTCAGCAGCCCTATT 118
 Db 13 GTACATCCACGATAGCAAAATCGCCTTGACGGTTGACGGTAATATCGGACTCAGCCCCAAA 72
 QY 119 TTAAACGT 126
 Db 73 CTGAACCT 80

Search completed: October 23, 2003, 08:19:54
 Job time : 6723 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2003, 06:19:14 ; Search time 508 Seconds
(without alignments)

9840.309 Million cell updates/sec

Title: US-09-868-987-1

Perfect score: 1864

Sequence: 1 atggacttcgcgattgttc.....atgacaattcagataatgc 1864

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 1287486

Minimum DB seq length: 5

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/1/pubpna/PCBUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 - 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25.4	1.4	88	10	US-09-983-965-5388
C 2	24.2	1.3	65	12	US-09-908-975-21214
C 3	24	1.3	65	12	US-10-032-585-23155
C 4	23.8	1.3	87	10	US-09-974-300-3986
C 5	23.6	1.3	60	12	US-09-908-975-7106
C 6	23.6	1.3	65	12	US-10-032-585-3029
C 7	23.6	1.3	98	12	US-10-308-891-25
C 8	23.6	1.3	98	12	US-10-308-891-86
C 9	23.4	1.3	60	12	US-09-908-975-5572
C 10	23.2	1.2	60	12	US-09-908-975-18757
C 11	23.2	1.2	60	12	US-09-908-975-22233
C 12	23.2	1.2	70	11	US-09-963-803-34
C 13	23.2	1.2	96	11	US-09-851-486-67
C 14	23.2	1.2	96	12	US-10-223-666-156
C 15	23	1.2	77	9	US-09-864-761-29497
C 16	22.8	1.2	65	12	US-10-032-585-560
C 17	22.6	1.2	60	12	US-10-334-672-2
C 18	22.6	1.2	60	12	US-09-908-975-21214
C 19	22.6	1.2	60	12	US-09-908-975-23155
C 20	22.6	1.2	60	12	US-10-334-671-2
C 21	22.6	1.2	65	12	US-10-032-585-1037
C 22	22.6	1.2	91	13	US-10-092-140-5
C 23	22.6	1.2	94	12	US-10-029-386-21155
C 24	22.6	1.2	96	11	US-09-851-486-61
C 25	22.6	1.2	96	12	US-10-223-666-150
C 26	22.6	1.2	100	11	US-09-849-928-15
C 27	22.6	1.2	100	14	US-10-066-960-15
C 28	22.4	1.2	65	12	US-09-908-975-27834
C 29	22.4	1.2	65	12	US-10-032-585-2537
C 30	22.4	1.2	86	9	US-09-864-761-18576
C 31	22.4	1.2	88	10	US-09-896-888A-15
C 32	22.2	1.2	91	14	US-10-137-036-47
C 33	22.2	1.2	93	10	US-09-960-352-4506
C 34	22	1.2	65	12	US-10-032-585-1310
C 35	22	1.2	96	10	US-09-878-574-7267
C 36	22	1.2	97	10	US-09-969-373-900
C 37	22	1.2	98	9	US-09-864-761-21839
C 38	22	1.2	98	12	US-10-308-891-24
C 39	21.8	1.2	65	12	US-09-908-975-1635
C 40	21.8	1.2	65	12	US-09-908-975-4780
C 41	21.8	1.2	65	12	US-10-032-585-586
C 42	21.8	1.2	65	12	US-10-032-585-2664
C 43	21.8	1.2	87	14	US-10-104-818-13
C 44	21.8	1.2	92	9	US-09-864-761-27613
C 45	21.8	1.2	92	14	US-10-005-338B-36

ALIGNMENTS

RESULT 1

US-09-983-965-5388/c
; Sequence 5388, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 5388
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 43-LIB34-027-Q1-E1-C4
US-09-983-965-5388

Query Match 1.4%; Score 25.4; DB 10; Length 88;
Best Local Similarity 58.7%; Pred. No. 7.7e+03;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY	211	GATGCTTTTGTCCGAGTCTCAGTGAAGAGAGATCTCTTCTGATCTTTGGGAAAAA	270
DB	88	GAGGCCACAGGTTATGGAGATAATCAGAGAGAGAGAGATGTTGGTGGGTGATATA	29
QY	271	ACAATGTACACAGG	285
DB	28	TCATGCAAAAAAGG	14

```
RESULT 2
US-09-908-975-29830
; Sequence 29830, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/09/032,585
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29830
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-29830

Query Match      1.3%; Score 24.2; DB 12; Length 65;
Best Local Similarity 66.0%; Pred. No. 1.4e+04;
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 816 AAAAATTGGCTGTTCTGGAAGTGTCTTTCTTTAGTTCGGTGTCTC 868
Db 13 AAAGAATTGGCCTGGATTGGTTGAGTTATCCCATTAAGCATCTTGTGTC 65

RESULT 3
US-10-032-585-3503/c
; Sequence 3503, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3503
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-3503

Query Match      1.3%; Score 24; DB 12; Length 65;
Best Local Similarity 60.9%; Pred. No. 1.5e+04;
Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1684 AGAACTTATCTCTCTTTATATTCACCACTCTGTTGTTTATGGTCCGTAAGA 1743
Db 65 ATGGAATTTAGCCTCTCATCATATTTAAACGCGTTGATGTTGATAAGGATTATCAATA 6

QY 1744 AAAT 1747
Db 5 GACT 2

RESULT 4
US-09-974-300-3986
; Sequence 3986, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085-500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3986
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-3986

Query Match      1.3%; Score 23.8; DB 10; Length 87;
Best Local Similarity 59.7%; Pred. No. 2.1e+04;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 331 GAGCGTATATTATAGATTGGAGGCGTCATCGCTTCGGGCGCTTCTTCTGAATCTTT 390
Db 1 GAGCGGAGGTATCGGACACGGAAGCGGTTTGCCTTTAATGTGTGTCGTCATCTCTT 60

QY 391*GCTTATC 397
Db 61 AATCATC 67

RESULT 5
US-09-908-975-7106/c
; Sequence 7106, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7106
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-7106

Query Match      1.3%; Score 23.6; DB 12; Length 60;
Best Local Similarity 76.3%; Pred. No. 1.9e+04;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 447 CTGGATTGTTCTTGTATGGGATGGCGCGTAGATGCA 484
Db 60*CTTGACTGCTCTGGCTATGGAAAGGCGCGTAGATCCA 23

RESULT 6
US-10-032-585-3029
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; TITLE OF INVENTION: Methods for Detecting Target Nucleic Acids Using Coupled Ligation
;
; TITLE OF INVENTION: and Amplification
;
; FILE REFERENCE: 7414.0020-01000
;
; CURRENT APPLICATION NUMBER: US/10/308,891
;
; CURRENT FILING DATE: 2002-12-02
;
; PRIOR APPLICATION NUMBER: US 09/584,905
;
; PRIOR FILING DATE: 2000-05-30
;
; PRIOR APPLICATION NUMBER: US 09/724,755
;
; PRIOR FILING DATE: 2000-11-28
;
; NUMBER OF SEQ ID NOS: 94
;
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 86
;
; LENGTH: 98
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: misc feature
;
; OTHER INFORMATION: complement of SEQ ID NO: 25
;
US-10-308-891-86

Query Match 1.3%; Score 23.6; DB 12; Length 98;
Best Local Similarity 58.6%; Pred. No. 2.5e+04;
Matches 41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1156 TGTGAGAAACAGCGCTAGATTCTCTACGGAACCTCTAAACGAAACGCAAAATTTGGTC 1215
Db 22 TGTGACGAAACGCGCATGTATCCATATACGGCAATCAAAATGAAGGAACCTTATGACCTAAGC 81

Qy 12168 AAAGGTAAAGC 1225
Db 82 AAAGGTAAAC 91

RESULT 9
US-09-908-975-5572
; Sequence 5572, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5572
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-908-975-5572

Query Match 1.3%; Score 23.4; DB 12; Length 60;
Best Local Similarity 67.3%; Pred. No. 2.1e+04;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 118 TTTAAACGTCCCATGAAATAATCATGCCAGTGTCTCAGGGAATTTACC 166
Db 28 TTTACCCCTTCAAGTTTCAAGTTTCACTGTCTCAGAGAGGTTTTCC 50

RESULT 10
US-09-908-975-18757
; Sequence 18757, Application US/09908975
; Publication No. US20030165843A1

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; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Directional Desoxynucleotide
US-09-963-803-34

Query Match      1.2%; Score 23.2; DB 11; Length 70;
Best Local Similarity 61.7%; Pred. No. 2.7e+04;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      1029 TTCAACAATTGGATCTTTCAGAAAGATCAAAATCTATTTTAGTGATAAAGCTTTAAGCT 1088
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      6 TTCAACACATACAAATTCAGTAGAGAGAAACTCATTACTCTTGAGAAACCTTAGAGGAT 65

RESULT 13
US-09-851-486-67
; Sequence 67, Application US/09851486
; Publication No. US20030036642A1
; GENERAL INFORMATION:
; APPLICANT: NEBOJSA JANJIC, LARRY GOLD
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
; ACID LIGAND COMPLEXES
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Brateschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,486
; FILING DATE: 08-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/991,743
; FILING DATE: 16-DECEMBER-1997
; APPLICATION NUMBER: 08/618,693
; FILING DATE: 20-MARCH-1996
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/479,725
; FILING DATE: 7-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX66
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid

```

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; FILING DATE: 20-MARCH-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rna
; FEATURE:
; OTHER INFORMATION: All pyrimidines are 2'-F modified
;
US-10-223-666-156

Query Match 1.2%; Score 23.2; DB 12; Length 96;
Best Local Similarity 44.7%; Pred. No. 3.2e+04;
Matches 38; Conservative 8; Mismatches 39; Indels 0; Gaps 0;

QY 737 ATGATAAACACCAATACACAGTTCATATGATGAATAAGTTCGTGGGATAAAGCAT 796
Db 8 AAGAAUAAAGCCUACACCCUGAGGNGGGAAGUAGUAGUUGGCGCCUACUACAU 67

QY 797 GATTTCTTCAGAGGATGCAAAAAC 821
Db 68 UGCGCUUCCAGAGGCGUCACAC 92

RESULT 15
US-09-864-761-29497/c
; Sequence 29497, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USE
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

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;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 29497
;; LENGTH: 77
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL161445.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.51
;; OTHER INFORMATION: NT HIT: AF239803.1, EVALUE 2.00e-03
;; OTHER INFORMATION: EST HUMAN HIT: C16927.1, EVALUE 6.00e-36
;; OTHER INFORMATION: SWISSPROT HIT: P42918, EVALUE 4.30e+00
US-09-864-761-29497

Query Match 1.2%; Score 23; DB 9; Length 77;
Best Local Similarity 63.6%; Pred. No. 3.2e+04;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 726 TCATGCTGTGGATGAATAAGACCAACATACACAGATTGCATATGATCAATAAGTT 780
Db 69 TGATGATGATGAGACTGTAATACATCGGAGAGATGCTGATGATAAGATTT 15

RESULT 16
US-10-032-585-560
;; Sequence 560, Application US/10032585
;; Publication No. US20030180953A1
;; GENERAL INFORMATION:
;; APPLICANT: Terry, Roemer D.
;; APPLICANT: Bo, Jiang
;; APPLICANT: Charles, Boone
;; APPLICANT: Howard, Bussey
;; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;; FILE REFERENCE: 10182-005-999
;; CURRENT APPLICATION NUMBER: US/10/032,585
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 8000
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 560
;; LENGTH: 65
;; TYPE: DNA
;; ORGANISM: Candida albicans
US-10-032-585-560

Query Match 1.2%; Score 22.8; DB 12; Length 65;
Best Local Similarity 66.0%; Pred. No. 3.3e+04;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 493 TGTATTCGAAGAATCCGAGAGAAATTTTATTTGCTCAAAAGCTTTAAAA 542
Db 9 TGTACTCCAAGAATACGACAGCAATTTATCTATCATATACTAATAAAAA 58

RESULT 17
US-10-334-672-2/c
;; Sequence 2, Application US/10334672
;; Publication No. US20030157646A1
;; GENERAL INFORMATION:
;; APPLICANT: Lanahan, Mike
;; APPLICANT: Koepf, Edward
;; APPLICANT: Kretz, Keith

;; TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed
;; FILE REFERENCE: SYNG-P01-001
;; CURRENT APPLICATION NUMBER: US/10/334,672
;; CURRENT FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: 60/344,523
;; PRIOR FILING DATE: 2001-12-28
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Forward Primer
US-10-334-672-2

Query Match 1.2%; Score 22.6; DB 12; Length 60;
Best Local Similarity 64.2%; Pred. No. 3.5e+04;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 587 GATTCTAACTTGACTACAGTATTGGCTTCAGCAGCTTCTTTCTCTCTAGATAC 639
Db 59 GATTCCAACTTCAATTCGGTTCAGATTGAGCCTCTCTTTCTCGAGAGATAC 7

RESULT 18
US-09-908-975-21214/c
;; Sequence 21214, Application US/09908975
;; Publication No. US20030165843A1
;; GENERAL INFORMATION:
;; APPLICANT: SHOSHAN, Avi
;; APPLICANT: WASSERMAN, Alon
;; APPLICANT: MINTZ, Eli
;; APPLICANT: MINTZ, Liat
;; APPLICANT: FAIGLER, Simchon
;; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE V
;; FILE REFERENCE: 36688-0005
;; CURRENT APPLICATION NUMBER: US/09/908,975
;; CURRENT FILING DATE: 2001-07-20
;; PRIOR APPLICATION NUMBER: US 60/287,724
;; PRIOR FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: US 60/221,607
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 32337
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 21214
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-908-975-21214

Query Match 1.2%; Score 22.6; DB 12; Length 60;
Best Local Similarity 68.9%; Pred. No. 3.5e+04;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1288 CATCTTGCTATGTGAGTTTGGCTTTGAATGCAATATGCTTT 1332
Db 52 CAGCCTGTCTTTTGGAGGCTACGGTTCCAATGACAATTTGCTTT 8

RESULT 19
US-09-908-975-23155
;; Sequence 23155, Application US/09908975
;; Publication No. US20030165843A1
;; GENERAL INFORMATION:
;; APPLICANT: SHOSHAN, Avi
;; APPLICANT: WASSERMAN, Alon
;; APPLICANT: MINTZ, Eli
;; APPLICANT: MINTZ, Liat
;; APPLICANT: FAIGLER, Simchon
;; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE V

; LENGTH: 65
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-1037

Query Match 1.2%; Score 22.6; DB 12; Length 65;
Best Local Similarity 75.4%; Pred. No. 3.7e+04;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 295 AGCATGCTGGCTTGGCAATGCTTATTGTGTTGATG 331
||| ||| ||| ||| ||| ||| ||| |||
Db 63 AGATAAATGTTTGCGCAATGCTTTTTTGTAGATG 27
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RESULT 22
US-10-092-140-5/c
; Sequence 5, Application US/10092140
; Publication No. US20020164801A1
; GENERAL INFORMATION:
; APPLICANT: McGill University et al.
; TITLE OF INVENTION: HUMAN AND MAMMALIAN DNA
; REPLICATION ORIGIN CONSENSUS SEQUENCES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SWABEY OGILVY RENAULT
; STREET: 1981 McGill College Avenue - Suite 1600
; CITY: Montr.al
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/092,140
; FILING DATE: 06-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,750
; FILING DATE: 09-Jun-1999
; APPLICATION NUMBER: 60/033,374
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: 60/047,322
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: C't., France
; REGISTRATION NUMBER: 4166
; REFERENCE/DOCKET NUMBER: 1770-162PCT FC/1d
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514 288-8389
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-092-140-5

Query Match 1.2%; Score 22.6; DB 13; Length 91;
Best Local Similarity 13.6%; Pred. No. 4.6e+04;
Matches 11; Conservative 47; Mismatches 23; Indels 0; Gaps 0;

QY 1591 AGTCACAACCTATCAGTTTGTATGCTTTTGTATTATAGCGGCCTCTCTCTTTAA 1650
|:::||||| |:::||||| |:::||||| |:::||||| |:::
Db 90 AMYKQWMMWWMMMTATSWTWAKMYCMRRYYTWAWKMCWAMTMMHKGTSSTYDW 31
|:::||||| |:::||||| |:::||||| |:::||||| |:::

Ov 1651 TTTTGCCATTATTATGACCATT 1671

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/ FILING DATE: 16-DECEMBER-1997
/ APPLICATION NUMBER: 08/618,693
/ FILING DATE: 20-MARCH-1996
/ APPLICATION NUMBER: 08/479,783
/ FILING DATE: 7-JUNE-1995
/ APPLICATION NUMBER: 08/479,725
/ FILING DATE: 7-JUNE-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barry J. Swanson
/ *REGISTRATION NUMBER: 33,215
/ REFERENCE/DOCKET NUMBER: NEX66
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (303) 793-3333
/ TELEFAX: (303) 793-3433
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 96 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: RNA
/ FEATURE:
/ OTHER INFORMATION: All pyrimidines are 2'-F modified
/ SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-851-486-61

Query Match 1.2%; Score 22.6; DB 11; Length 96;
Best Local Similarity 44.7%; Pred.No. 4.7e+04; Indels 0; Gaps 0;
Matches 38; Conservative 8; Mismatches 39;

QY 737 ATGATAAGACCCACATACACAGTTGCATATGATGAATAAAGTTCGTGGGGATAAAGCAT 796
DB 8 AAGAAUACGCUAACCCUGAGUGGGGGAAGUUGAAUCAGUUGGGCGCUCUACUCAU 67

QY 797 GATTTCTTGAGAGGATGCAAAAAC 821
DB 68 UCGCCUUCGACAGGAGGCUACAAC 92

RESULT 25
US-10-223-666-150
/ Sequence 150, Application US/10223666
/ Publication No. US20030180744A1
/ GENERAL INFORMATION:
/ APPLICANT: LARRY GOLD et al.
/ TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
/ TITLE OF INVENTION: LIGANDS TO GROWTH
/ TITLE OF INVENTION: FACTORS
/ NUMBER OF SEQUENCES: 304
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Swanson & Bratschun, L.L.C.
/ STREET: 8400 E. Prentice Avenue, Suite 200
/ CITY: Englewood
/ STATE: Colorado
/ COUNTRY: USA
/ ZIP: 80111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/223,666
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/973,124
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/08014
/ FILING DATE: 30-MAY-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/458,423

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1 FILING DATE: 04-May-2001
2 CLASSIFICATION: <Unknown>
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 08/952,793
5 FILING DATE: <Unknown>
6 APPLICATION NUMBER: 08/479,724
7 FILING DATE: 07-JUNE-1995
8 APPLICATION NUMBER: 08/472,256
9 FILING DATE: 07-JUNE-1995
10 APPLICATION NUMBER: 08/472,255
11 FILING DATE: 07-JUNE-1995
12 APPLICATION NUMBER: 08/477,829
13 FILING DATE: 07-JUNE-1995
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Barry J. Swanson
16 REGISTRATION NUMBER: 33,215
17 REFERENCE/DOCKET NUMBER: NEX40C/PCT
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (303) 793-3333
20 TELEFAX: (303) 793-3433
21 INFORMATION FOR SEQ ID NO: 15:
22 SEQUENCE CHARACTERISTICS:
23     LENGTH: 100 base pairs
24     TYPE: nucleic acid
25     STRANDEDNESS: single
26     TOPOLOGY: linear
27     MOLECULE TYPE: RNA
28     FEATURE:
29     OTHER INFORMATION: All C's are 2'-NH2 cytosine
30     FEATURE:
31     OTHER INFORMATION: All U's are 2'-NH2 uracil
32     SEQUENCE DESCRIPTION: SEQ ID NO: 15:
33 US-09-849-928-15
34
35 Query Match      1.2%; Score 22.6; DB 11; Length 100;
36 Best Local Similarity 68.9%; Pred. No. 4.8e+04;
37 Matches 31; Conservative 0; Mismatches 14; Indels
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; APPLICATION NUMBER: 08/479,724
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,256
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/472,255
; FILING DATE: 07-JUNE-1995
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX40C/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-066-960-15
Query Match 1.2%; Score 22.6; DB 14; Length 100;
Best Local Similarity 68.9%; Pred. No. 4.8e+04;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1345 CGCTTTAATTCAGACCTTTGGCTACCTGTGAGCTCTTTAT 1389
DB 59 CGTTCTAATTCAGTACACTTTCGATTCCCGCGAGTCTTGAT 15

RESULT 28
US-09-908-975-27834
; Sequence 27834, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27834
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-27834
Query Match 1.2%; Score 22.4; DB 12; Length 65;
Best Local Similarity 66.7%; Pred. No. 4.2e+04;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 766 TATGATGAATAAGTCTGTGGGGTAAGCATGATTTCTTCAGAGGATG 813
DB 18 TAGGAACAATCAGTGATCCGGTGACAGCCTGGGTCTTTAGAGGCTG 65

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RESULT 29
US-10-032-585-2537/c
; Sequence 2537, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2537
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-2537
Query Match 1.2%; Score 22.4; DB 12; Length 65;
Best Local Similarity 62.5%; Pred. No. 4.2e+04;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 680 ATTTCTCTCAATGTTTACGGCTCTTTTCATGACTAAATTTTCTTCATGCTGTG 735
DB 57 ATTCITTTTGAATACTTTCGTTTCGTCGTATCTTTTTCGCTTAATAGTG 2

RESULT 30
US-09-864-761-18576
; Sequence 18576, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18576
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009484.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EST HUMAN HIT: AL038099.2, EVALUE 2.00e-26
; OTHER INFORMATION: SWISSPROT HIT: P11369, EVALUE 2.00e-04
; OTHER INFORMATION: NT HIT: A0229043.1, EVALUE 4.00e-21
US-09-864-761-18576

Query Match 1.2%; Score 22.4; DB 9; Length 96;
Best Local Similarity 62.5%; Pred. No. 5.3e+04;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 688 TTCAATGTTTACGGCTTTTCATGACTAAATTTTCTTCATGCTGTGGATGAATA 743
DB 31 TGCATGATTTTCTCTTTTATGCTGAGTAGTATCCATGGTGTGTGTATA 86

RESULT 31
US-09-896-888A-15/c
; Sequence 15, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REFERENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US/09/048,911
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/049,946
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: promoter sequence of the ACMNPV ion gene
US-09-896-888A-15

Query Match 1.2%; Score 22.2; DB 10; Length 88;
Best Local Similarity 54.2%; Pred. No. 5.7e+04;
Matches 45; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 439 AGCACTCGTGGATTTCTTCTATGGGATGGCGGTAGATGCAAAATTTCTTGTATT 498
DB 86 ACCGATTGTAGAGATTGTACTGTATATGGAGTGTCCAGCAAAAGTGAACCTTTTTCATT 27

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QY 499 CGAAAGAAATCCGAGAGGAATTTT 521
DB 26 GCAGAAAAAATTCATTTTAAATTT 4

RESULT 32
US-10-137-036-47/c
; Sequence 47, Application US/10137036
; Publication No. US20030101478A1
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036c4
; CURRENT APPLICATION NUMBER: US/10/137,036
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. US20030101478A1 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-137-036-47

Query Match 1.2%; Score 22.2; DB 14; Length 91;
Best Local Similarity 64.7%; Pred. No. 5.9e+04;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 797 GATTTCTTCAGAGATGCAAAAACTTTGGGCTGTTCTCGGAAGTCTTTT 847
DB 75 GAATTCCTCGGAGAACCAACAGACTGTGCCATTACCGGCTTTGTAGTT 25

RESULT 33
US-09-960-352-4506
; Sequence 4506, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4506
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-BOVMS1-022-Q1-E1-E7
US-09-960-352-4506

Query Match 1.2%; Score 22.2; DB 10; Length 93;

```

Qy	1071	GT	1072
Db	66	GT	67

```

RESULT 37
US-09-864-761-21839
Sequence 21839, Application US/09864761
Patent NO. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED
FILE OF INVENTION: GENE EXPRESSION ANAL
FILE REFERENCE: Aescima-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006659
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006655
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006658

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Qy 1156 TGTCAGAAACAGCGCTAGATTTCTCTACGGAAACTCTAAACGAAACGCAAAATTTTGGTC 1215

[illegible]

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RESULT 41
US-10-032-585-586/c
; Sequence 586, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: BO, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 586
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-586

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RESULT 42
US-10-032-585-2664
US-10-032-585-2664, Application US/10032585
; Sequence 2664, Publication No. US20030180953A1
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2664
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-2664

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RESULT 43
US-10-104-818-13/c
; Sequence 13, Application US/10104818
; Publication No. US20030087398A1
; GENERAL INFORMATION:
; APPLICANT: Varigenics, Inc.
; TITLE OF INVENTION: A Method for Analyzing Polynucleotides

```

RESULT 44

US-09-864-761-27613
; Sequence 27613, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

Search completed: October 23, 2003, 09:33:10
Job time : 508 secs

;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 27613
;; LENGTH: 92
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004457.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.72
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.58
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.65
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69
;; OTHER INFORMATION: EST HUMAN HIT: AA806461.1, EVALUE 1.80e-02
;; OTHER INFORMATION: NT HIT: AF045555.1, EVALUE 1.20e-02
US-09-864-761-27613

Query Match 1.2%; Score 21.8; DB 9; Length 92;
Best Local Similarity 56.2%; Pred. No. 7.6e+04;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 584 TTGTGATTCTTAAGTACACATATGGCTCAGCAGCTCTTTCTTCTAGATACAGGG 643
DB 1 TTGTCTTTGACACTAAGTCTTCTGACATCAGCATCAGTTTCTCATCACTAAAGGA 60
QY 644 CCTATTAAAGGT 656
DB 61 GTAGTTAAATGTT 73

RESULT 45
US-10-005-338B-36/c
;; Sequence 36, Application US/10005338B
;; Publication No. US20030044895A1
;; GENERAL INFORMATION:
;; APPLICANT: DENEFILE, Patrice
;; APPLICANT: ROSIER-MONTUS, Marie-Francoise
;; APPLICANT: PRADES, Catherine
;; APPLICANT: ARNOULD-REGUIGNE, Isabelle
;; APPLICANT: DUVERGER, Nicolas
;; APPLICANT: ALLIEMETS, Rando
;; APPLICANT: DEAN, Michael
;; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENES
;; FILE REFERENCE: ABCA5, 6, 9, 10
;; CURRENT APPLICATION NUMBER: US/10/005,338B
;; CURRENT FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: US 60/263,231
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: FR 00403440.1
;; PRIOR FILING DATE: 2000-12-07
;; NUMBER OF SEQ ID NOS: 217
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 36
;; LENGTH: 92
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-005-338B-36

Query Match 1.2%; Score 21.8; DB 14; Length 92;
Best Local Similarity 56.2%; Pred. No. 7.6e+04;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 1349 TTAATTTCATGACCTTTTGGCTACCTGTGCGAGTCTGTTTATAGCAGATTCTTTTGAAG 1408
DB 91 TGAATAACAGAGATCTTTTCGCAATCTTTTCCCAATTTTAGTTCATGCATCTTAGAA 32
QY 1409 AAAATTCAATAG 1421
DB 31 CAAAACGAATAG 19

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